Enterococcus faeca Partial Enterobact Enterococcus faeca

Staphylococcus Staphylococcus

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Staphylococcus aur Enterococcus faeca
Enterococcus faeca
S. pneumoniae deri
                                                                                      Streptococcus pneu Escherichia coli p S. epidermidis gen Enterococcus faeca (glutamicum codin Stabhylococcus aur C.glutamicum phosp (glutamicum phosp S. epidermidis gen S. epidermidis gen S. epidermidis gen Enterococcus faeca Enterococcus faeca
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99US-0150310.
99DE-1042095.
99DE-1042097.
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   Corynebacterium glutamicum
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Brevibacterium lac
C.glutamicum phosp
S. epidermidis gen
Enterococcus faeca
Streptococcus pneu
Escherichia coli g
Streptococcus pneu
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                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Staphylococcus aur Staphylococcus aur Gene encoding a su Enterococcus faeca HIV codon altered

Enterococcus faeca DNA encoding a S. DNA encoding a Pts

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers

AAV52334 AAQ55752 AAV52163 AAT47502

92.5 12.5 9.9 9.9 7.1 7.1

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1527 1515 1492 1412.6 1107.4 190.6 151.2 126.6 108 107.8

Query

Score

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14: 115: 117: 119: 119: 120: 120:

100.0 99.2 97.7

Haberhauer G;

Zelder O,

Schroeder H,

В,

Pompejus M, Kroeger WPI; 2001-080989/09

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Staphylococcus aur Staphylococcus aur Enterococcus faeca

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                            phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome,
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                                                                                               Length 1527;
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                        present invention relates to Corynebacteium glutamicum
                                                                                                           Indels
                                                                             BP; 304 A; 392 C; 430 G; 401 T; 0 other;
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Conservative 0; Mismatches
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                                                                                                                               acid synthesis; vitamin; saccharide;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium to producing amino acids, nucleic acids, vitamins, saccharides and organic acids particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                 Yokoi
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Ozaki A;
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                                                                                                                 H, Ando
Ikeda M,
                                                                        (KYOW ) KYOWA HAKKO KOGYO KK
              07-APR-2000; 2000JP-0159162
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Ξ Gaps Length 349980; ij Indels 22; ; 0 DB Pred. No. 0; 0; Mismatches 99.2%; Score 1515; 99.9%; Pred. No. 0; Query Match 99.2 Best Local Similarity 99.9 Matches 1526; Conservative

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111266 CGTTTCGGCGCGAATGACTTCCTGGGCGCCG-GTATTGGTATGCGATGGTGTTCCCCGAG 111208 CTCATGGCATCTGCGCCGTTCGCGTTCTTGCCAGTGTTGGTTTGGTTTCACCGCAACCAAG 111267 ctcatggcatctgcgcgttcgcgttcttgccagtgttggtttggtttcaccgcaaccaag cgtttcggcggcaatgagttcctgggcgccgcgtattggtatggcgatggtgttcccgag cttggtgaacggctacgacgtggccgccaccatggctgcgggagatgccaatgtggtc Db 111326 61 121 g ò ò

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110128 110728 110608 1140 720 900 110607 CTTCATCGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTTTAATATCAA 110127 TCGCACCAAGGCTGAGGATGGTTCCAATGTGGATATCTTGATGCACTTGGATTCACACTTGGATACACT 110067 AGTAAACCTCAACGGCACGCACTTTAACCCGCTGAAGAAGAGGGGGGATGAAGTCAAAGC 110847 CACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTTAACCAGGGTGGATC 110667 TGTTCTTGGTATTACGGAGCCTGCGATCTTCGGTGTAACCTTCGCCTGCGCTGGCCGTT 109947 CACGCCGATTGTTGTTTCGAATTACAAGAAAACCGGGACCTGTAAACACTTACGGTTTGGG tgttcttggtattacggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccgtt cttcatcggtatcggtaccgcagctatcggtggcgctttgattgcactctttaatatcaa tegeaceaaggetgaggatggtteeaatgtggatatettgatgeacattggtttegacae agtaaacctcaacggcacgtttaacccgctgaagaagcagggggatgaagtcaaagc 1321 aggggagctgctgtgtgaattcgatattgatgccattaaggctgcaggttatgaggtaac AGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAAC cacgccgattgttgtttcgaattacaagaaaccggacctgtaaacacttacggtttggg ACCATAAGTTGAAACCTTGAGTGTTCG 109801 accataagttgaaaccttgagtgttcg 1527 661 901 1201 1261 721 110007 1501 110427 1081 1381 g QQ g g g g a g 염 à ö δ ò ò δ ò ò ò ò ö ŏ ð á ð

RESULT

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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one withbut the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.
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                                                                                                                                                                                                                                                                                                           01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                Pompejus M,
                                                                                                                                                                                                                                  09-APR-2001
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03-SEP-1999;
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The present invention relates to Corynebacteium glutamicum phosphonolopyruvate: sugar phosphotanasferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, alted bacteria, as reference points for mapping C. glutamicum genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gttcgcaccaaggctgaggatggttccaatgtggatatcttgatgcacattggtttcgac 1258
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Pred. No. 0;
0; Mismatches
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103-104; 144pp; English
                                                                                                                                               Sequence 1109 BP; 236 A; 278 C; 303
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The polypeptides may also be used to assay for other inhibitors of their extructy and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts containing them which are used to produce hosts calls which express the polypeptides. The polypeptides (II) via the production of vectors polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria.
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                             gcaggggagctgctgtgtgaattcgatattgatgccattaaggctgcaggttatgaggta
                                                                                                                          gcaggggagctgctgtgtgaattcgatattgatgccattaaggctgcaggttatgaggta
                                                                                                                                                                       accacgccgattgtttcgaattacaagaaaaccggacctgtaaacacttacggtttg
                                                                                                                                                                                                                        S. epidermidis genomic polynucleotide sequence SEQ ID NO:3464
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sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
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                                                                                                                                                 Length 2913;
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                                                                                                                                               Score 190.6; DB 22; Length
Pred. No. 2.7e-46;
0; Mismatches 364; Indels
                                                                                          Sequence 2913 BP; 1072 A; 480 C; 419 G; 942 T; 0 other;
                                                          no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                               12.5%;
55.0%;
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Matches 468; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and fouuse in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1970 ttaatgggttcgttgtggcaagtcttggtaatgtttggtatgcattgggggctttgtacca
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                                                                                                                                Enterococcus faecalis; contig; detection; Enterococcal infection;
vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 1848 A; 944 C; 1256 G; 1779 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.9%; Score 151.2; DB 20;
48.5%; Pred. No. 2.2e-34;
live 0; Mismatches 533;
                                                                                                        contig SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 389-392; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                         CA;
                            BP.
                                                                                                                                                                                                                                                                                                                                                         Kunsch
                           AAX12968 standard; DNA; 5840
                                                                                                        faecalis genome
                                                                                                                                                                                                                                                                           97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                              HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                    98WO-US08985
                                                                              (first entry)
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                                                                                                                               faecalis;
                                                                                                                                                                                                                                                                                                                                                         Dillon PJ,
                                                                                                                                                                        Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-045171/04.
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                                                                                                        Enterococcus
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                                                                                                                                                                                                                                                                            14-NOV-1997;
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16-MAY-1997;
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                                                                                             tatggcgtgactttaccattgaaaaaaccatttattgcagcttgtattggtggcggtatc 2269
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aatategeeceagggtgeggeatgtttggeagtgttetteetggegaagagtgaaaagete
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 31 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. (AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the cucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a proces comprising: (a) screening of the sequences in SEQ ID NO:1 to 391, identifying members of the 11brary which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating man, DNA or CDNA produced from an organism, amplifying nucleic acid molecules from the members; or (b) isolating contain sequence is homologous to amplification on and isolating the amplified sequences. The computer contains and isolating the amplified sequences. The computer contains and also and a computer based system for identifying the numbers of the computer of the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments of the S. pneumoniae genome of commercial importance, or
                    S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical compositions and vaccines for S. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                   Fannon
                                                                                                                                                                                                                                                                                                                                                   Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1179-1182; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                 Dillon PJ,
                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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                      pneumoniae;
                                           computer readable medium;
                                                                                      Streptococcus pneumoniae
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Rosen CA;
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                      Streptococcus
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Kunsch CA,
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                                    27;
   DB 19; Length 3895;
                                      Indels
                                    619;
8.3%; Score 126.6; DB 1
llarity 47.1%; Pred. No. 3.9e-27;
Conservative 0; Mismatches 619
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AAO55752 standard; DNA; 3615

AAQ55752/c ID AAQ557

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| | AGTTAAATGGCTCTTCGGTGCAATTTTTGGCGCCCCTCTACGCTCCATTTGTCATCACGG
                                      totgoaccagtccttcccgccaattgagctggagctgttt---aaccagggtggatcctt
                                                              CCTATGGCCAATGATTGCTCTTTCTAATATTGCTCAAGGCTCAGCCGTGTTTGCCTATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2495 TCACACCATIGCTATGTCTGATGGTTATCACCCGTCACCTTTCTGCTGGTGGGGCCGC 2436
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                                                                             Probe; S.aureus; S.epidermis; E.faecalis; P.aeruginosa; E.coli; K.pneumoniae; E.cloacae; clinical sample; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                             infectious disease -
HindIII cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 108; DB 15; Length 3 Pred. No. 1.3e-21; 0; Mismatches 590; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3615 BP; 966 A; 962 C; 805 G; 882 T; 0 other;
                                                                                                                                                                                                                                                                  Ξ,
                                                                                                                                                                                                                                                                                                            Probe for identifying bacteria causing consists of a DNA fragment obtained by pathogenic bacterial genomic DNA
                                                                                                                                                                                                                                                                  Uehara
                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 62-64; 100pp; Japanese.
                                                         coli genomic probe EC-24
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Similarity 46.28;
                                                                                                                                                                                   93WO-JP00936.
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                                 (first entry)
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                                                                                                                                                                                                                                                                                                           Probe for identifying
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                                                                                                                                                                                                                                                                                      WPI; 1994-035086/04.
                                                                                                               Escherichia coli.
                                                                                                                                                                                                                             (FUSO ) FUSO
(OHNO/) OHNO
                                                                                                                                                                                   07-JUL-1993;
                                                                                                                                                                                                         07-JUL-1992;
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                                                         Scherichia
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                                                                                                                                                            20-JAN-1994
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           AAQ55752;
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Best Local S
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2015 CCTTTGGTTTGCCAAGTATTTTCACCTTCATGCAAACCATCCCGTGAACGGGAATTGATT 1956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tccaggcacctttgaccggtgaagctattgcactgagcagcgtcagcgatgccatgtttg 1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cggtgagtggaaagattgtgggtggcattcccatctggccatgctttcgcagttcgcacca 1208
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                                                                                                            gtatcggtaccgcagctatcggtggcgctttgattgcactctttaatatcaaggcagttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caggaacgaccaaagccgaagcagcacccgcagaattttcaaacgattccaccatca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               909 tttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgcctg
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vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae genome fragment SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1449 aagcgggagccaacctgctcaacgtc 1474
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us-09-604-231-1.rng

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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)

Crecorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the incleic acid molecules from the members; or (b) isolating many, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification molecules whose nucleotide sequence is homologous to amplification the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences: The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or an analysing and solating decompleted and sequences of commercial importance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                     Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9769 BP; 2918 A; 2141 C; 1792 G; 2916 T; 2 other;
                                                                                                                                                                                          Fannon
                                                                                                                                                                                          Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 318-324; 1409pp; English
                                                                                                                                                                                     Dillon PJ,
                                            97WO-US19588
                                                                                         96US-0029960
                                                                                                                                                                                     Cho1 GH,
Rosen CA;
                                                                                                                                        (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                          WPI; 1998-272225/24
                                            30-OCT-1997;
                                                                                         31-OCT-1996;
                                                                                                                                                                                     SC,
CA,
                                                                                                                                                                                     Barash
Kunsch
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ŝ 8979 GACCTCTTGGTAACACCATTCGTGACACTTTTGGTCATGTCTATCCTTGGACTCTTTGTC 8920 8679 GTTGGTGTTAAAACAAAAATCCAAAACTGAAAACACTTGCTTTCCCGGCTGCTCTTTCT 8620 361 421 Gaps gacttcctgatcactccagtgctgacgttgctgctcaccggattccttacattcatcgcc 362 attggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacagggactttat 8859 AGCATGCCATTIGGTCTTGGTGGTTCTTGATTGGTGGGGGTTCACCAATTGATCGTCGTG 482 actggtctgcaccagtccttcccgccaattgagctggagctgtttaaccaggg---tgga AACCCATTCAACGCTATCATCACAGCTGCTATGACAGCTCAAGGTGCTGCTACTGTTGCG gtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgcttcaggtgtctcc 8919 ATTGGACCAGTTTTCCACGTTGTTGAAAACTACATCCTTATTGCTACAAAGCGATTCTT 539 tccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcggcatgtttggca 36; DB 19; Length 9769; 7.1%; Score 107.8; DB 19; Length 46.6%; Pred. No. 2.6e-21; Live 0; Mismatches 597; Indels Best Local Similarity 46.6 Matches 552; Conservative Query Match 302 8739 ò q ò 셤 ò g ð g ò

Protaminobacter rubrum.

8053 1019 tecaccateatecaggeacetttgaceggtgaagetattgeactgageagegteagegat 1078 8161 8101 gcaggggagctgctgtgtgaattcgatattgatgccattaaggctgcaggttatgaggta 1378 GCTGGCGATGTTCTTGGAACATTTGACTCAAACAAATCGCTGCAGCTGGACTTGATGAT 7933 ACAACAATGGTTATCGTTACAAATACAGGTGACTACGCTTCAGTAGCTCCAGTCGCAACA 7873 scr operon; scrA; sucrose metabolising enzyme; sucrose isomerase; reduced metabolism; non-cariogenic sugar; trehalulose; palatinose; decomposition; monosaccharide; improved yield; disaccharide; ds. 1139 ttagtttctccggtgagtggaaagattgtggtggcattcccatctggccatgctttcgca 719 ttcttcatcggtatcggtaccgcagctatcggtggcgctttgattgcactctttaatatc CCAGTCTTCTCAAGTGGAGCTATGGGACAAGGTATCGTTGTGAAACCAAGCCAAGGCGTG ACTGTATCTATGAACGGTGACGGTTTTGAAACAAAAGTTGCTCAAGGTAATAAGGTGAAA TICTICCITICATIGATIGCTGGTGCAATCGGTGGTGGATTGGCTTCTATCCTTGGACTT 779 aaggcagttgcgttgggcgctgcaggtttcttggggtgttgtttctattgatgctccagat 8499 GCTGGTACTGGTAATGGTATCACCATCATCCCTGGTACAATGCTTTATGTTGGTAACGGA 8439 CAACTTCCACAATACCTTCTTATGGTAGCTGTATCATT------TGCCCTT gcttatggcctttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgct ccagtgcctgcaggaacgaccaaagccgaagcagaagcacccgcagaatttcaaacgat GAAACACTIGI - - - AACTCCTATCGTCGGTGATGTTGTCGCTCTTGCTGATGAC GTCTATGCACCAGCTGATGCTGAAGTTTCAATTGCCTTTCCAACAGGGCACGCTTTTGGT gttcgcaccaaggctgaggatggttccaatgtggatatcttgatgcacattggtttcgac 8100 TTGAAAACAAGAAATGGTGCT------GAAGTTTTGATTCATGTTGATTGAT accacgccgattgtttcgaattacaagaaaaccggacctgtaaacacttacggtttg atggtcatgttcttggtgtgtgtgcagttgttaccttcttcatcgcattcggcgcagtt 8394 GGTTTTGCTCTTACTTACATGTTTGGTTACG---AAGATGAAGTAGACGCAACTGCAGCT 8337 GCAAAACGAGCTGAAGTGGCTGAAGAAAAAGAAGAAGTTGCGCCAGCAGCTCTTCAAAAT acagtaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatgaagtcaaa 7872 GGTTCAGTTGCTAAGGGGGATGCTGTGATCGAAGTGAAAATCTAA 7828 ggcgaaattgaagcgggagccaacctgctcaacgtcgcaaagaaa 1483 Partial P. rubrum scrA gene region. BP AAT47502 standard; DNA; 465 (first entry) AAT47502; 839 626 1079 7992 8619 1199 1319 1379 1439 8559 899 8160 8052 7932 1259 g οy g ò 셤 δ g οy Ωp οχ Dp ογ g ò Dp Ω g ò g δ g ò qq ò q ŏ g 

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                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                       Staphylococcus aureus contig SEQ ID #56.
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1741..1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell with reduced sucrose metabolism activity - providing high yields of n trehalulose and palatinose
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                                                                                                                                                             27-JUN-1996;
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CO-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a kit for the immunodetection of Saureus in a sample. Saureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyellitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences
                                                                                                                                                                                                                                                                                                                                                           the se bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence...27000
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in the production of
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stored on computer readable medium and used
anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 422-438; 3271pp; English.
                                                                                                                                                                                                                                                             "these bases
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                                                                                                                                                                                       gattaaataaagtcgttcacgattcgataaaaatgttggtcgttggacccgtagcgcttt 11592
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtattacatctggtgttacatttatattccaacatgcaggatggcttggcggagcaatat 11712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512
                                                                                                                                                                       153 tggctgcgggcgaaatgccaatgtggtccctgtttggtttagatgttgcccaagccggtt 212
                                                                                                                                           Gaps
(and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11893 tggttaaagaagaaggcttggcattaacatcttgtatttctggtatgtaggtgttactg
                                                                                                                                                                                                                                                                                                   273 tectgeacaagegaeteaagggeactgeagaetteetgateaeteeagtgetgaegttge
                                                                                                                                                                                                                                                                                                                                                                                 213 accagggcaccgtgcttcctgtgctggtggtttcttggattctggcaacgatcgagaagt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --gaaaagctcaagggccttgcaggtgcttcaggtgtctccgctgttcttggtattacgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         teggtetggtetacteaceaategteateactggtetgcaceagtecttecegceaattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctaatatcgcccagggtgcggcatgtttggcagtgttcttcctggcgaagagt-----
                                                                                                                                          15;
                                                                                                            Length 30246;
                                                            Sequence 30246 BP; 9663 A; 4436 C; 6386 G; 8791 T; 970 other;
                                                                                                                                          Indels
                                                                                                                                          0; Mismatches 313;
                                                                                                            DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12013 cgtcttgtgtattgggggcaatcgttggtatgaataa 12049
                                                                                                           Score 86.2; DB 18 Pred. No. 1.3e-14;
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                                                                                                           5.6%;
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                                computer readable medium.
                                                                                                                                           Matches 309; Conservative
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                                                                                                                             Local Similarity
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                                                                                                            Query Match
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AAX13576 standard; DNA; 474 BP

AAX13576

(first entry)

19-MAR-1999

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of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can demonstance the second for the summer of the polypeptides. The new DNA sequences can be used the their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
in the production of
                                                                                                                                                                                                                                                                                                                                                                                                           Kunsch CA;
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                                                                                                                                                                                                                                                                                                                                                                                                           Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide(s) and proteins derived stored on computer readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1918; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Dillon PJ,
                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                               97EP-0100117.
                                                                                                                                                                                                                                           96US-0009861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homologues of any of the computer readable medium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC, Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4PI; 1997-374922/35
                                                                                                                                                           07-JAN-1997;
                                                                                                                                                                                                                                           )5-JAN-1996;
EP786519-A2
                                                                                    30-JUL-1997
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1; Gaps Score 76.4; DB 18; Length 465; Pred. No. 1.2e-12; 0; Mismatches 146; Indels 1 5.0%; Conservative Similarity Local Simi nes 175; Query Match Best Loca Matches

ggtgcggcatgtttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgca qq ð

581

71 tctgccgcagtattttcagcattacttggtattacagaaccggctatgtttggtgtt-ac 129 701 cttcgcctgcgctggccgttcttcatcggtatcggtaccgcagctatcggtggcgctttg 760 g ò

130 ttaaaactaagatatccatttattggcgctatcgttggatcaggtattggttcagcatat 189 190 attgctttcttcaaggttaaagcaatcgcattaggaactgctggattgccaggatttatt 249 761 attgcactotttaatatcaaggcagttgcgttgggcgctgcaggtttcttggggtgttgtt ŏ g

g

250 tcaatcaatccagtacatgcaggatggttacactactttgttggtatgacaatatcattc 309 tctattgatgctccagatatggtcatgttcttggtgtgtgcagttgttaccttcttcatc 821 ð qq

881 gcattcggcgcagcgattgctt 902 

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982 nucleotide sequences isolated from the Enterococcus faccalis genome. AAX1298 to AAX13019 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faccalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faccalis in samples. They can also be used for progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faccalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faccalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                   Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 474 BP; 134 A; 85 C; 86 G; 163 T; 6 other;
                                                                                                   Enterococcus faecalis; contig; detection; Enterocovaccine; attenuation; computer readable medium; ds
                                                                   Interococcus faecalis genome contig SEQ ID NO:639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1887; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                             97US-0044031.
97US-0046655.
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                                                                                                                                                      Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-045171/04.
                                                                                                                                                                                       W09850555-A2
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                                                                                                                                                                                                                                                                                             14-NOV-1997;
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16-MAY-1997;
                                                                                                                                                                                                                         12-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection.
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176 tggtccctgtttggtttagatgttgcccaagccggttaccagggcaccgtgcttcctgtg 235 47 tggaatatttttggataccatgttgcacaaacaaactatgcctaccaagtaattccggta 106 236 ctggtggtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggc 295 356 atcgccattggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacaggga 415 Gaps 296 actgcagacttcctgatcactccagtgctgacgttgctgctcaccggattccttacattc ; 0 Length 474; Indels Pred. No. 5.3e-12; 0; Mismatches 173; DB 20; 4.9%; Score 74.2; DB 2: 50.7%; Pred. No. 5.3e-12 Query Match
Best Local Similarity 50.7'
Matches 178; Conservative ò pp ò qq ò d δλ

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The present sequence comprises a partial DNA sequence from the scr operon containing the scrA gene region. The scr operon encodes sucrose metabolising enzymes, in particular sucrose isomerase. Cells containing at least one DNA sequence encoding a protein with sucrose isomerase activity, and having reduced ability to metabolise sucrose, or their extracts, optionally in an immobilised form, are used to produce non-carlogenic sugars, especially trehalulose and/or palatinose. During production of the non-carlogenic sugars, decomposition of sucrose to monosaccharides (which are difficult to separate from the product) is minimised, so the yield of the disaccharides is improved.
                                   416 ctttatgatttcggtggtccagtcggcggtctgctcttcggtctggtctactcaccaatc 475
                                                          scr operon; scrA; sucrose metabolising enzyme; sucrose isomerase; reduced metabolism; non-cariogenic sugar; trehalulose; palatinose; decomposition; monosaccharide; improved yield; disaccharide; ds.
227 acagttattggtcccacaatgttattactatctaatggaatcacagatgctattgtttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell with reduced sucrose metabolism but with sucrose isomerase activity - providing high yields of non-cariogenic sugars, esp.
                                                                                                       476 gtcatcactggtctgcaccagtccttcccgccaattgagctggagctgttt 526 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 347 gttatgactggtcttcatcagtcatttcctgcaatcgaaacacagttactt 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 357 BP; 46 A; 121 C; 107 G; 81 T; 2 other;
                                                                                                                                                                                                                                                                                                                                              Partial Enterobacter sp. scrA gene region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SUED-) SUEDZUCKER AG MANNHEIM/OCHSENFURT.
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                                                                                                                                                                                                                                    AAT47505 standard; DNA; 357 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stegmaier
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4.7%; Score 71.6; DB 18; Length 357; llarity 53.1%; Pred. No. 2.7e-11; Conservative 0; Mismatches 134; Indels 0,

Query Match Best Local Similarity Matches 152; Conserv

183 29

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247 teggeceggecegtegegeteggegaeggtatttegtttatecteageaegettatea 306
ttggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacagggactttatg
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Search completed: March 22, 2002, 08:53:35 Job time: 4584 sec

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Description

AE006222 Pasteurel M7678 Vibric algi x69800 s.xylosus s 254245 B.subtilis D83967 Bacillus su D86417 Bacillus su 299108 Bacillus su

AE004395 Vibrio ch M22711 Streptococc

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Run on: ĕ

Sequence:

Title: Perfect :

Searched:

Database

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1 (bases 1 to 1527)
Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G. Orynebacterium glutamicum genes encoding phosphoenolpyruyat e: sugar phosphotransferase system proteins
Patent: WO 0102583-A 1 11-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers
1. 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum.
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX069134 1527 bp DNA
Sequence 1 from Patent WO0102583.
AX069134 GI:12579016
                       AX127152
AX122988
AX069136
PDCRAFOPER
PPSURFOP
                                                                                                                                                                                     AX144742
AP001514
AF229829
AP001513
AP001508
KPSCRYAB
EAM250722
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BSU34876
BACISPQ
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AE007479
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AE007557
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        Length DB
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Query
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SOURCE
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TITLE
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AP003365 Staphyloc AF269422 Staphyloc AX144742 Sequence AX144742 Sequence AX14742 Sequence AP001513 Bacillus AP001513 Bacillus AP001508 Bacillus AT050722 Erwinia a M81772 Erwinia ach U34876 Bacillus st U37921 Alkalophiol X67750 S. typhimuri J03006 B. subtilis X73124 B. subtilis

25-JAN-2001

PAT

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Corynebacteriaceae;
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Ozaki,A.
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Corynebacterium.
1 (bases 1 to 349980)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M.
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and
Novel polynucleotides
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Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria;
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Sequence 7068 from Patent EP1108790.
AX127152 AX114121
AX127152.1 GI:14041140
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Patent: EP 1108790-A 7068 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
1. 349980
/organism="Corynebacterium glutamicum"
//db_xref="taxon:1718"
//note="Seq 1 to long (3.309.400) split 3.700.001 3.049.980"
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Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
Povel polynucleotides
Patent: EP 1108790-A 2904 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
Corynebacterium glutamicum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Ma.	Oy Dp	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Oy Dp	Qy Db	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Qy Db	Qy Dp	Qy Dp	Qy

caccatcatccaggcacctttgaccggtgaagctattgcactgagcagcgtcagcatgc 1080	AX069136 1109 bp DNA PAT 25-JAN-2001 AX069136 AX069136 AX069136 AX069136 AX069136 AX069136 AX069136 AX069136 AX069136 AX069136.1 GI:12579018 Corynebacterium glutamicum. Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Corynebacterium glutamicum genes; Corynebacteridae; Actinomycetales; Corynebacterinee; Corynebacteridae; Corynebacterium glutamicum genes encoding phosphoenolpyruvat e: Sugar phosphotransferase system proteins I (bases Itolio) Corynebacterium glutamicum genes encoding phosphoenolpyruvat e: Sugar phosphotransferase system proteins BASF AKTIENGESELISCHAFT (DE) Location/Qualifiers I. 1109 /organism="Corynebacterium glutamicum" /db_xref="taxon:1718" /codon_start=1 /kransl_table=11 /kransl_table
Oy 1021 of Oy 1081 of Oy 1081 of Oy 1081 of Oy 1141 of Oy 1201 of Oy 1201 of Oy 1321 of Oy 1321 of Oy 1381 of	AXO69136 DECUS DECUS DECUS DECUS DECUS DECUS ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE JOURNAL FEATURES CDS CDS

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OKLLTKLRLEDAKQRLSTSNNSVQSIANMYGYKDSFTFSKAFKRYSGASPSYYRKSIG
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Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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alpha-glucosidase; fructokinase; insertion element; permease; rafi
gene; rafR gene; raffinose operon; regulatory protein; scrA gene;
scrB gene; scrK gene; scrR gene; sucrase; sucrose-6-phosphate;
ACCACGCCGATTGTTGTTTCGAATTACAAGAAACCGGACCTGTAAACACTTACGGTTTG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                         transport protein.
Pediococcus pentosaceus (strain PPE1.0) DNA; Insertion sequence
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                                         /function="regulation raffinose-operon"
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Pediococcus pentosaceus raffinose operon genes.
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gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMDFLKVLSDIFIPIVPALVAGGLLMALNNVLTAEHLFMAKSVVEVYPGLKGIAEMIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 21838;
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Best Local Similarity 58.8%; Pred. No. 8e-67;
Matches 539; Conservative 0; Mismatches 364;
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IILLLETNLGGLYAKNAMI YLVVFAILY ITMDI FYSFKDVGFWSMLPSLTTDSRERE
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us-09-604-231-1.rge

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Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G. The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0 Unpublished
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     Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                             Direct Submission
Submitted (27-APR-1994) Leenhouts K. K., Institute for Biological
Sciences, Department of Genetics, Kerklaan 30, Haren, The
Netherlands, 9751 NN
On May 26, 1994 this sequence version replaced g1:475962.
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14545 CCACGTTCTGTCCGTGGCGATGGGTCCCGCATCAGTCATCGATTGCTTTC 14486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14965 TGGTCCCGTCTTACGAACGGTGAGCGATTAACTAACGGTTTAGTAGGCTTATATAA 14906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14905 CAGCACCGGCTGGATTGGTATGGGAATCTTTGGTTTATTATTATTCTGCAATTGTTATTAC 14846
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                                                                                                                                                                                                                                               gtttggtttagatgttgcccaagccggttaccagggcaccgtgcttcctgtgctggtggt
                                                                                                                                                                                                    cttcctgatcactccagtgctgacgttgctgctcaccggattccttacattcatcgccat
                                                                                                                                                                                                                                                                                                                                                15025 CTTCACGTTTACCCCGATGTTTGCCATTGTGATTACTGGTTTCCTAACTTTTACAATCGT
                                                                                                                                                                                                                                                                                                                                                                                  tggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacagggactttatga
                                                                                                                                                                                                                                                                                                                                                                                                                                                  tttcggtggtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtcatcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 gggtggatcettcatettcgcaacggcatetatggetaatatcgcccagggtgcggcatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgcttcagg
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                                                   ttcggcggcaatgagttcctgggcgccgtattggtatggcgatgttcccgagctt
                                                                                                                 124 ggtgaacggctacgacgtggccgccaccatggctgcgggcgaaatgccaatgtggtccct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832 tccagatatggtcatgttcttggtgtgcagttgttaccttcttcatcgcattcggcgc
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P.pentosaceus (PPE1.0) sucrose and raffinose operons
232771
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PPSURFOP/C
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/translation-"MNHQEVADRVLNAIGKNNIQAAAHCATRLRLVIKDESKIDDQAL
DDDADVKGTFETNGGYQIIIGPGDVDKVYDALIVKTGLKEVTPDDIKAVAAGQNKNP
LMDFLKVLSDIFIPIVPALVAGGLLAALNNVLTAEHLEMAKSVVEVYFGLKGIAEMIN
AMASAPFTPILLGFSATRFGGGPVLGATAGTAGTAGTSVATTMAAGKNVY
WNWFGLHVAQAQYQQCQVLPVLGVAFILATLEKFFHKHIKGAPDFTFPMFAIVTTGFT
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YFTTHPVDAIGIGSFGPIGVNPHDPRYGYITTTPKPGWGDFDFLGHLKSQFNIPLYWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDVNEAAYGESMIGIAKDVPNSIYMTIGTGVGAGVISQNHIFNGRTHTELGHMRLNRL
PODDFKSCHOFYHDICLEGLAAGPAVGKRTGKRGKDIPVDDPVWPIITDYIAQACVNLT
VAFAPDKIILNGGVMNQRQLFPMIREKFAAYLNGYEEVPPLDDYIVPAGLGNNSGIAG
GLLLAQAALKNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function "enzyme II of the PTS system, sucrose specific"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15324 ATGGCTAGTGCGCCGTTTACTTTCTTGCCAATCCTCTTAGGATTTTCAGCAACGAAGCGC 15265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15205 AGTTAACGGCTATAGCGTTGCAACGACCATGGCAGCCGGCAAGATGGTTTACTGGAACGT 15146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15085 CGCTTCATTCTAGCTTGAAAAATTCTTCCATAAACACATTAAAGGGGGATTTGA 15026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 gtttggtttagatgttgcccaagccggttaccagggcaccgtgcttcctgtgctggtggt 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 ttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgcaga 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15145 CTTTGGGTTACACGTTGCACAAGCCGGCTATCAAGGCCAAGTGCTCCCAGTCTTAGGCGT
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                                                                                                                                                                                                                                                                                                                                                                   /function="fructose 6-phosphotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 287.6; DB 1;
Pred. No. 8e-67;
0; Mismatches 364;
                                                                                                                                                                /standard_name="terminator 2"
                                                                                                                                                                                                                                                                                                                                   /standard_name="fructokinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:P43470"
                                                                                                                                                                                                     complement(10727. .11593) /gene="scrK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(13852. .15989)
/gene="scrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(13852. .15807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="fructokinase"
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/db_xref="G1:475967"
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/db_xref="GI:475968"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name="enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=experimental
                                                                                                            /rpt_type=INVERTED
10681. .10716
                                                                                                                                                                                                                                                                          complement(10727.
/gene="scrK"
/rpt_type=DIRECT
10397. .10443
                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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/note="IR2"
                                                                                     /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                         /citation=[1]
                                                                                                                                                                                               /citation=[1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="scrA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /citation=[1]
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58.8%;
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Best Local Similarity 58.87
Matches 539; Conservative
                            repeat_unit
                                                                                                                                            terminator
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LINHLRLSWSPGMIAHEFKLATKSIYNWLNOGRIGFSLNDLPBHGVRGRTNVDORSKYN
OSLGRSIEQRPWMFNQRNRIGDFELDTVVGPRGHSKAVLLTLIDRKSRFLWAYRLKDR
TYATVNREALFKELTFNGPVHSFTVDRGTEFSGLVSLESQYGIKTYYCHAYTPADVVV
NNALIGIYVVPILKGLVLSTLVVLKI"
10396...10442
                                                                                                                                                                TGNKALDNRAVSLVTLIIMVLRIVELFIDPFIGNAIDRTKNSPGHFRPWVVVGGTVSS
IILLLFTNLGGLYAKNAMIYLVVFAILYITMDIFYSFKDVGFWSMLPSLTTDSRERE
                                                                                                                                                                                                                   KTATFARLGST IGGGLVGVLVWPAVIFFSAKATSTGDNRGWFIFALIICLIALISAWG
VGGTREVSDSTRIKDDTVGVMEIFRALAKNDJCLMAALATFGYGOINILGSLEVY
YFTY IMGRR KSFSILLSIIN FLGILATSLFPYLSKKFSKRGYFAGCLYFMLGGIAIFT
IAGSNLWLVLLAATWFGFPQQMVFLVVLMVITDSVEYGQLKLGHRDESLALSYPRELID
                                                                                                                                                                                                                                                                                                                                   KFGGAISNGVVGQIAIISGMTTGATASSITAAGQLHFKLTMFAFPALMLLIAIGIFSK
QIFLTEEKHAEIVAELERTWRTKFDNTTDQVAEKVVTSLDLATPIAGQVIPLAQVNDP
                                                                                                                                                                                                                                                                                                                                                                                                     LRGTGFISYVEEGQHVQQGDELLEFWDPTIKQAGLDDTVIMTVTNSTEFTMMDWLVKP
GQARKATDNILQLHTKA"
5976. .8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /traislation="MSLITYDOANRYFHLHNOTLSXIFAVEQGGTLSHLXFGGHUDHY
HGELRYPRYDRGFSGNLPGSTDRTFSRDTLPKEYSTAGEMDYHLPAAIVRHTDGANAL
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YRRYQGVRIGDHAVNEWQLDFTDROFFTITLDFGGAHANERHPERGSINYGTGT
FGSLRGTSSHOMNPFLALVDHTTFESGDAYGFNLYSGNHAFELEKOQLOQLIGUGT
INSYNFWQLKAGATFQTPEVLWYYNKGLNAMSQAYHLIRERVYRSEFKNQERPIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNNWEATFFDFNEAKLKPIVDEAKQLGIEMFYLDDGWFGHRDDDNSSLGDWQVDHRKF
PQGLNHFVKYVHEQGLKFGIWLEPEMISYDSKLYQQHPDYLMQVPGRSPSPSRNQYIL
DLGRQAVRNNIFDQLDQLLKSKQIDYIKWDMNRHLSDIYSVALPPERQGEVYHRYVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYELLERLITAYPHILEGGCSGGGRFDAGMAYYMPQIWASDNTDAWARLTIQYGTSL
PYPISLATAHYSVSPNQOTGRETSMSTRAVAASGVLGYELDLTQLSSADKQIYOKOV
VQYKQIRPLIQFGGFYRLKSPITSNQAMMYYSPQODEAIWYFNLTSYAQPSLTKTK
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                                                                                                                                      /translation="MQEEHNYKWVGGRLIYGFGAKGNDAFYSILSGYLIIFITSHLFD
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enzyme II sucrose protein; fructokinase; sacA gene; sacB gene; sacK
gene; sacR gene; sucrose-6-phosphate hydrolase.
Lactococcus lactis.
Lactococcus lactis
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Luesink, E.J., Marugg, J.D., Kuipers, O.P. and de Vos, W.M.
Characterization of the divergent sacBK and sacAR operons, involved
In sucrose utilization by Lactococcus lactis
J. Bacteriol. 181 (6), 1924-1926 (1999)
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Lactococcus.
15025 CITCACGITTACCCCGAIGTITGCCAITGGAITACTGGITTCCTAACTTITACAAITGT 14966
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Location/Qualifiers
1. 5800
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Lactococcus lactis cremoris sucrose gene cluster.
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Luesink, E.J.
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                                                                                                                                                                                                                    ttcaggtgtctccggctgttcttggtattacggagcctgcgatcttcggtgtaaccttcg
                                                                                                                                                                                                                                                                                                                         4085 ACTAAAATATCCGTTCTTTATTGCTCTTGGGGCTTCAGCAATTGGTTCATTATTATGG
                                                                                                                                                                                                                                                                                                                                                               actetttaatateaaggeagttgegttgggegetgeaggtttettgggtgttgttetat
                                                                                                                                                                                                                                                                                                                                                                                                                                      tgatgetccagatatggtcatgttettggtgtgtgeagttgttacettetteategeatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cggcgcagcgattgcttatggcctttacttggttcgccgcaacggcattgatccaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4325 TAAACAGAATGC------AACAACTCAATACCAACCTGAGAAAGTTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1006 attttcaaacgattccaccatcatccaggcacctttgaccggtgaagctattgcactgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4550 TCACGCTTATGGTATAAAAACAAAAATGGAGGT------GAAGTTCTTTACA
                                                                                                                                              ggcatgtttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgcaggtgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4430 TGATGTAAGTGACCCTGTTTTCTCAAAAGAATTATGGGAAAAGGTATTGCAATCAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cattggtttcgacacagtaaacctcaacggcacgcactttaacccgctgaagaagcaggg
   tggtctgcaccagtccttcccgccaattgagctggagctgtttaaccag--
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AE004395 AE003853
AE004395.1 GI:9658068
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                                                                                                                                                                                                                                                                                                                                                                                                                               /product="fruccokinase"
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PALEGINLKIKYPFFTALGASAITGSLEMGLFHVLAVSLGSAGLIGFTSI KASTALAPAGVSALLGITE
ISTFISFLIAFVVTSIYGRRNEAKSITKEKNKQNATTQYQPEKVIIDPVKSGELLAPI
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SASYNEILPLSENVDIKVGEKILLLIN
                                                                                      VMALVKLLSDIFVPLIPALVAGGLIMALNNALTAEHLFATKSLVEMFPMWKGFADIVN
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   sucrose protein"
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Pred. No. 7.2e-57;
0; Mismatches 647;
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                                                                                                                                                                                                                                                                                                                                                                              number="2.7.1.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNFYLAYSLFTKE'
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=?
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4838. .5720
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/gene="sack"
4848. .5720
/gene="sack"
/EC_number="?
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51.1%;
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Best Local S:
Matches 725,
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ORIGIN
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                                        Bacteria: Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 10264)
Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L.,
Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.,
Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D.,
Ernolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D.,
Nierman, W.C. and White, O.
                                                                                                                                                                                                                                                                                                                                                                                                         Heidelberg, J. F. Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, R.E., Read, T.D., Tettelin, H., Richardson, D., Sellers, P., Wonathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., Whiter, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Direct Submission Braser, C.M.

Submitted (14-JUN-2000) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA
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TFANAPFVYLPVLLAFSASRKFGGNPFLGAALGMLMVHPDLLNGWGFGSASVSGTVPT
WNILGFEIEKVGYQGSVLPVLVSAYILAKIENGLRKIVPSVVDNLLTPMLAIFITGFL
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LADIVTTGGTFIFPIAAMSNIAQGAAALAVGVMTKETKLKGVAIPSGVTALLGITEPA
MFGVNLKLRYPFIAAICGAALASAFITLFNVKAQALGAAGLPGIISINPQQIGYYIMG
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SIESGYQMAKQAYLDYPQLDGLFCATDRLAVGAIKALQELGVHVGQQVKLLGVGNDEL
AYVSNPPLSTFNYAFDKAGENAAKMLLERIAGRGQEMSKVVLTFQNIQRETCPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MDYPVIAKQLLESLGGKSNIQALAHCATRLRLVLNDETQINESA
IESLQGVKGQFKVAGQYQIIFGSGIVNQVYAEMAKLTGLVEMSTNDVASAGAEKQNWA
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KEIEYIQIFNQKRVEGIVFYATHLDQPLVHAIQHSAVPVVLVGQDGSLYNIPSIVHDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="PTS system, sucrose-specific IIBC component"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L14685 PID:289864; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="sucrose operon repressor ScrR, putative"
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    10264
    organism="Vibrio cholerae"

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2922. .456°
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/gene="VCA0654"
1854. .2846
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/gene="VCA0654"
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/translation-"MALLESNHILRSDSMSRVWLTGDAVVDLIPDGQQHYLKCPG
GAPANVAVAIARLCSRAFEGRYGNDPFGREWQQTLTDEQVDCQHLYEDPVHRTSTVV
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OMKEVGGYVSPDPNLREEVWSEPQELQATVMRAVGLADVVKFSEEELQFLTGTQSIEE
GLQAIADFQIPLVVYTGAKGALVYTPNSRQIVSGRAVKPIDTTGAGDAFVGGLLYRL
SVAQDHHNQATLLDAVKWANGCGALATTQKGAMTALPNQAALXAFLE"
6008. 7546
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WVKQFLANENAHVSSPYGIRLIQGSHIIVPRIHDEPQAYILQNEDKRIVFVIPYLDDYS
WIGTTOVEYKGDPRKYAITDARROYLISIVNKHFMRETARSDIIAEFSGVRPLCDDES
NSPQAITRYDLLDQAAFLSIEGGKLTYRKGEAAMKHLAPFPKMKAPWTA
DAPLPGGENFDYAALKNQLVAAPLFFFFFSVIERWLRSYGSRTYQLLAGYTGIEDLGIA
FSGELYQREIDYLCEKEFARHAQDIFWRRSKLGLAHDTSVVEEVESYLQQKFHAEQPL
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TKSGGFYWVDAYVTDIYQQGQLTGYQSVRVKAERKWVEIATKAYQALLAAEKAGKKIQ
FKLHTSLRYALLLGALMSPALAHGFQAPEQWQWLASLLPAGVLGLLFRQELVRTPQQL
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FDSHGYFESGHAVSHQDDLWLFYTGNTRLGVDRQRQTMQCAARNANGFFEKLGPVIRC
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DYGYWWECPDNFELQGEAFFYGWQNLLGAGTAANGCRAYYBHTIENGNRIFRATHWHPDKLYGDELG
WPLDEGFDFYAPQTAGGARFYLCGWMGLPDETQHPSCDQGWIHQUTALRELBALLQ
RIYOHPLRELDTLQSEPHTLLLSDNYTELKTSFALQYTLPWGCELRLWQNTQYRVTL
TLDAENQLLTRLDRSATQIRGGPTIRELKTSFALQYTLPWGCELRLWQNTQYRVTL
RIFTPRDASGISLHGSVDAKLYYMAPASAPFNLEVNVQP"

COMPLEMENT (4600.5651)
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/db_xref="G1:9658074"
/translation="MYTFALIKITLEQQAEMSAYTPSAQQEVLVGDHDQLVSTTDLKG
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TTQEYHQALAAQNSNIQAVTQATDÄVESAAERVSSHTHSAHQLIDQVQDHCAETKHSI
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KDFASATSSASSKLVHGGLRYLEHYEFRLVSEALAEREVLLKKAPHIVTPMRFRLPHR
PFLRPAWMIRAGLFLYDNLGKRTSLPASHKVNLKAGSVTKPEWQIGFEYSDCWVDDAR
                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLLDTLLELAGGINNVTRILAPQGQVVLALKHPPLVPHLPDDVS
LQSVLGEWQLSVQRTAEVSDQQLAAIGKAIAERQKLETLPYQTALDCPYRPLWHISPP
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/protein_id="AAF96558.1"
/db_xref="GI:9658073"
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/note="similar to GB:M74035 PID:155269; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="methyl-accepting chemotaxis protein"
                                                                                                                                                                                                      /product="sucrose-6-phosphate dehydrogenase"
/protein_id="AaR96556.1"
/db_xref="GI:9658071"
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/protein_id="AAF96557.1"
/db_xref="G1:9658072"
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/6008. 7546
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PEMGYAPQRKTSVMPNAMTOPRSASYEDLROYLLSNGIQHEVVPGDYPMIKLNNTVRF
ETGSARVSMASKQMLDTVARFLATESGIDIVLEGHTDNTGSEKLNDKLAERRANAVKA
ALVOSRVAQNAIYTREGEBVVPACTNSTKNGRACNRRVEIRFILASN"
complement(10068..10190)
NVTHONLORLATQAESAALTTLKLSDQAQQVGQLMTEIGGIAEQTNLLALNAAIEAAR
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Pred. No. 1e-51;
0; Mismatches 387; Indels
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/note="ldentified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                           protein'
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/protein_id="AAF96561.1"
/db_xref="GI:9658076"
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complement(10068. .10190)
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/db_xref="GI:9658075"
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/transl_table=11
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55.4%;
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/translation="MDYSKVASEVITANGKDNLVAAAHCATRLRLVLKDDSKVDQKAL
DKNADVKGTFKTDGQYQVIIGPGDVNFVYDEIIKQTGLTEVSTDDLKKIAASGKKFNP
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IMAAAPFWLPILVGISAARFRGANGFGASIGMIVAPGAANIIGLAANAPISKAAT
IGAYTGFWNFFGLHYVQASYYYQVIFVLVAWALLSILEKFFHKRLPSAVDFFFPLLS
VIITGFLTFIVIGPVWKEVSDWLTNGIVWLYDTTGFLGMGVFGALYSPVVMTGLHQSF
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Location/Qualiflers
1. .2508
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Sato,Y., Poy,F., Jacobson,G.R. and Kuramitsu,H.K.
Characterization and sequence analysis of the scrA gene encod
enzyme Ilscr of the Streptococcus mutans phosphoenolpyruvate-
dependent sucrose phosphotransferase system
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agggtggatccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcggcat
                                 CTTTAGCTGTGGGTGTGATGACGAAAGAGACCCAAACTCAAAGGGGTCGCGATTCCTTCGG
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complement(<1. .28)
/note="sucrose-6-phosphate hydrolase (scrB)"
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/strain="GS-5"
/db_xref="taxon:1309"
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/db_xref="G1:153801"
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/db_xref="GI:7272364"
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223. .2217
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SSIPFYVVCELISFAIAFAVTYGYGKTKAVDVFAAEAAVEEAIEEVQEIPEEAASAAN
KAOVTDEVLAAPLAGEAVELTSVNDPVFSSEAMGKGIAIRPSGNIYVAPVOGTVQIAF
DTGHAYGIKSDNGAEILIHIGIDTVSMEGKGFEQKVQADQKIKKGDVLGTFDSDKIAE
AGLDNITMEIVINTADYASVETLASSGTVAVGDSLLEVKK"
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PAIETQLISAFQNGTGHGDFIFVTASMANVAQGAATFAIYFLTKDKKMKGLSSSGVS
                                                                            /note-"pot. transcription termination signal; putative" 401\ c 513 g 854 t
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                                                                                                                                    Length 2508;
                                                                                                                                 Score 230.8; DB 1;
Pred. No. 1.9e-51;
0; Mismatches 717;
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al Similarity 50.1%;
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                                                                                                                                                               GATGTCTTTGCTGCTGAAGTGCTAGAAGCTATTGAAGAAGTGCAAGAATTCCA 1722
                                                                                                                                                                                                                                                                                                                            CTIGCIGGIGAAGCIGIIGAATIAACCICIGITAAIGACCCIGITITITICIAGCGAAGCA 1842
                    GGTTTTCTTGGTTTCCTTTCTATTAAGGCAAGTTCTATTCCATTTTATGTAGTCTGTGAA 1602
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St. Paul, MN
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Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                             gccgaagcagaagcacccgcagaattttcaaacgattcca.--ccatcatccaggcacct
                                                                                                                                                                                                                                                                                                                                                                       1843 ATGGGTAAGGGGATTGCTATCAAACCTAGTGGTAATACAGTTTATGCACCGGTTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggttccaatgtggatatcttgatgcacattggtttcgacacagtaaacctcaacggcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GIGCGGAGATICTTATICATATIGGTATIGATACAGTATCAATGGAAGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cactttaacccgctgaagaagcagggcgatgaagtcaaagcaggggagctgctgtgtgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ttcgatattgatgccattaaggctgcaggttatgaggtaaccacgccgattgttgtttcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttgttaccttcttcatcgcattcggcgcagcgattgcttatggcctttacttggttcgc
                                                                                              1603 TTAATCAGTTTTGCTATAGCTTTTGCAGTAACTTATGGCTATGGTAAGACGAAGGCTGTT
                                                                                                                                       cgcaacggcagcattgatccagatgcaaccgctgctccagtgcctgcaggaacgaccaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATTTGAACAAAAGTTCAAGCAGATCAAAAATTAAAAAAGGTGACGTTCTCGGAACA
                                                                                                                                                                                                                                                    GAAGAAGCTGCTTCTGCAGCAAATAAGGCACAAGTTACTGATGAAGTTCTTGCGGCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2191 GATAGCTTACTTGAAGTTAAAAATAAGAAATATTATCAGAAAGGCGTAAGGT 2244
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the
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Pasteurella multocida PM70
GI:12722266
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Pasteurella multocida
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Zhang, Q. and Kapur, V.
Direct Submission
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WHIFGLEIERVGYQGTVIPVLVASWVLATLEKNLRKVVPSFLDNLITPLFALFITGĞL
LAEVIGPIGREAGSLISTGITWLYDTIGFVGGAIFGTLYAPPIVITGHHQTFIAVETQL
LAEVARTGGTFIFPIAAMSINAQGAACLGAAYWKDAKVRGIAVPSGISALLGITEPA
MFGYNLRYRY PFISAMIGAGISSAVALFNVKAIALGAAGLFGIPSIKPDSLAMYCVG
MLISASIAFTLTVILGKRAQLKAE"
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LIMNSPAEMKTVVNQVVALADVLKFSEEELLFLTDSDTLSDATAKLTQHYPDKLIIVTL
GKGARTYTYLGGKSQLVSSKKALIPVDTTGAGDAFVSGLLFGISQVKNWQNPTALVEII
KQANACGALATAKGAMSALPNKQDLDAFLAE"

1988 C 2212 g 2962 t
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                                                                                                                                                                                                                                                                                     IENIEGVKGGFAVAGGYQIIFGSGTVNKVYAALSKLLGIGDMTTSEVAAAGTEKGGLL
QRLVKGLADIFVPIIPAIVAGGLLMGIHSMLTAKGFFVEEKNVVDLYPAIADLVDFIN
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/db_xref="GI:12722274"
                                                                                                                                                                            /protein_id="AAK03930.1"
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/db_xref="G1:12722275"
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/gene="scrR"
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/note="PM1848"
complement(7557. .9056)
/gene="scrB"
complement(4859. .6283)
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/transl_table=11
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                                                                                                                                              /product="PtsB"
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1158. 1400
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1158. 1400
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YOGHTLKKERGYALISPRSIGFCPGAEGGPRKRPHYYHYRLAEMLQQOYAIRL
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                                     multocida"
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/gene="PM1843"
complement(2259. .3224)
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/gene="rfaF"
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/gene="PM1845"
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                                     /organism="Pasteurella
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/gene="PM1842"
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WNILGFEIQYVGGSSVLPYLYSAFILAKVELGLKAVGYNSKOKKWGIAIPSFIAIETQL
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1998. . 2921
/gene="scrk"
1988. . 2921
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
Batteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
Blatch,G.L., Scholle,R.R. and Woods,D.R.
Nucleotide sequence and analysis of the Vibrio alginolyticus gencrose uptake-encoding region
Gene 95, 17-23 (1990)
91071601
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                                                                                                                                                                        /organism="Vibrio alginolyticus"
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                                                                                                                                                                                                                               /gene="scrA"
393. .1832
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M76768 M30194
enzyme II-sucrose protein; fructokinase; sucrase-encoding; sucrose uptake-encoding.
Vibrio alginolyticus DNA.
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                                                                                                                                                                                                                 5682 TITCIGAIGGCIGGAAITAIGCACIGACACICGCIAAAGGCAAIAIICAAIATIGGCAIA
                                                                                                                                                                                                                                                                                                                                                  CCTCTTGGGTCTTAGCAACCTTGGAGAAAACCTACGTAAAGTCGTTCCGTCATTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                          ACACATTAGGATTCGTGGGGGGTGCCATTTTTGGTACACATTAGGACCCATTGTTATCA
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                                     5741 ATTTGGCGGTAATCCATTCTTAGGAGCGGCAC-TTGGCATGCTATTAGTGCACCCAGCAC
                                                                                                                                                                                 tggtgaacggctacgacgtggccgccaccatggcgggcgaaatgccaatgtggtccc
                                                                                                                                                                                                                                                     tgtttggttttagatgttgcccaagccggttaccagggcaccgtgcttcctgtgctggtgg
                                                                                                                                                                                                                                                                                         5622 TCTTTGGTTTAGAAATTGAACGTGTCGGCTACCAAGGTACAGTTATCCCCGTTCTTGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5022 TTAATGTTAAAGCCATTGCTTTAGGCGCTGCGGGCTTGCCGGGTATCCCCTCAATTAAGC
                                                                                                                                                                                                                                                                                                                           243 tttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgcag
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   13;
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   Indels
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Auf der Morgenstelle 28, 7400 Tuebingen 1,
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frames.
                                                                                                                                                                                                                                                                     1356 GGTATGCATCACACCTTCATTGCGATTGAAACTCCAACTTCTTGCGGATATTGCAACGACG
                                                                                                                                                                                                                   713 tggccgttcttcatcggtatcggtaccgcagctatcggtggcgctttgattgcactcttt
                          1176 AACCTTTTAACGCCATTACTGGCGATTTTCATAGCGGGTTTGTTGACGTTTACTGTCGTC
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                                                                                                                                                               ggtctgcaccagtccttcccgccaattgagctggagctgttt------aaccag
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S.xylosus scrA gene and unidentified open reading
X69800
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1. .2655
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Mol. Gen. Genet. 241 (1-2), 33-41
94049686
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Direct Submission
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FEATURES
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YGIAMILAFIVAFGYTYALSYRKYRNIEA"
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Pred. No. 5.6e-46;
); Mismatches 359;
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                                                                                                                                                                                                                               complement(<1. .121)
/note="ORF3"</pre>
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1053. .2495
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/Producial alea (CAA91014.1")
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AIVLIVPFAGTYAYGRFKHK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tre, domains B and C" corresponds to position 1 of x80203"
Submitted (27-SEP-1995) Dahl M. K., University of Erlangen-Nuernberg, Lehstuhl fuer Mikrobiologie, Staudtstr. Erlangen, Fed. Rep. of Germany, 91058 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'GTEAAFTLPDSLAPDEWKAEVLLTNDEAREGLQNMTVAHMSPLFIV"
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/function="phospho-alpha-(1,1)-glucosidase"
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/note="position 1136 c
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167. .1579
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/gene="treA"
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Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                            2015
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      gtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaagggcactgca
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Dahl, M.K.
Direct Submission
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TESRHRIDKFRFVDFFRRGK"
838 c 1088 g 1095 t
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Pred. No. 1.5e-44;
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YLRPPRGVFGSFYVLETTRKGYTVFWSVARVDWKINNQKGKYAYDHMIKQAHPGAI

YLLHTVSRDNAEALDDAITDLKKQGYTFKSIDDLMFEKEMRLPSL"
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(passes 1 to 22197)
Sekjauchi, 7.
Direct Submission
Submitted (08-MRR-1996) to the DDBJ/EWBL/GenBank databases. Jun Sekjauchi, Textlle Science and Technology, Shinshu University, Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano Japan (E-mail:)sekigu@glptc.shinshu-u.ac.jp, Tel:0268-21-5344,
                                                                                                                                                                                                                                                                                           20-NOV-1997
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Bacillus subtilis, Bacillus/Clostridium group;
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Nucleotide sequence analysis of B. subtilis cromosome
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C DNA, 74 degree region
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7. Croganism="Bacillus subtilis"
7. crossis="8.7.37"
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complement(1754..1778)
complement(1777..1962)
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Bacillus subtilis genomic
D83967
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2090. .2109
2107. .2571
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2 (bases 1 to 22197)
Sekiguchi, J., Yamamoto
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                                                                                1549 ATACGCGTATGGC 1561
895 gattgcttatggc
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D83967/c
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JOURNAL
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AUTHORS
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SCHOPLEMENT (8396 ... 8415)

COMPLEMENT (8422 ... 8742)
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complement (9228. .9247)
                                                                                                                                                                                                                                                                                                 translation="MLMVAVLSVGASACFMARFAFRVLFVMASAFFRMLGHHDIPPTS"
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9433. .9648
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GALCFFIAGVPPSPYVIGGCFFIAGMAVGSTFTLGISYWTDLLPPHLLDFAGNLLCGIT
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complement(4109. .4903)
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CDS
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RBS RBS CDS

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NLIAGTAFTFLPALIGWSAVKRFGGNPLLGIVLGVMLVHPDLLNAWGYGAAEQSGEIP
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FGVNLRYRFPFILAWVSSGLAGMYISSQGVLASSVGVGGVPGIFSIMSQYWGAFAIGM
TVLLYVPFAGTYAYARFKHK"
COMPLEMENT (1466. .1483)
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GRODRIIRSTATTKNLLKKEWBEVYKDMEVHVVPIVTIEQGGGVLXKTISH"
                                                                                                                    DDBJ/EMBL/GenBank databases. Junichi
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                                                                          Direct Submission
Submitted (09-JUL-1996) to the DDBJ/EMBL/GenBank databases. Junichi
Sekiguchi, Textile Science and Technology, Shinshu University,
Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano 386,
Japan (E-mail:jskigu@@iptc.shinshu:u.ac.jp, Tel:0268-21-5344,
                                                                                                                                                                                                                                                                      Yamamocto, H., Uchiyama, S., Nugroho, F.A. and Sekiguchi, J. Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis, spenome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein 97417488
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/organism="Bacillus subtilis"
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/db_xref="GI:2443218"
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/transl_table=11
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/trans1_table=11
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        Bacillus/Staphylococcus
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                                                        Sekiguchi, J
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Bacillus subtilis (strain:AC327) DNA.
Bacteria: Rirmicutes: Bacillus/Clostridium group;
                                                                                                                                                                                                 TCTATTCGGCCTAGAGGTGCAGAAGTCGGCTATCAGGCCCAGGTGCTCCCAATTTTGCT 20146
                                                                                                                                                                                                                                                                                                        CGGTTCGGCGCCAATCCGCTTCTCGGCATTGTGC-TCGGGGTTATGCTCGTGCATCCTGA 20266
                                                                                                         TTTGCTGAATGCGTGGGGATATGGCGGCGGCAGAACAAAGCGGAGAGATCCCGGTATGGAA 20206
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FFPDLKKDGLYDKSIIVMFOPHYGISBHNRKAMAKVLGKDETTDYDNAGAQRYPLFIH
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PKYTKISGKYYDTKTGKELDESEVDKSEDSLVKKELEMSDKIINGDLLRFYEPKGFKK
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                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLSFLOKLGKSFMLPIAVLPAVGIILALGREDVFNIPFVYQAGT
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GEWMLGLGGIGAGIFGLFNRLLIPLIGLHVLNNIFWFQFGEYNGVTGDLARFRAKDPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              925 CGGTTCGGCGGCAATCCGCTTCTCGGCATTGTGC-TCGGGGTTATGCTCGTGCATCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866 TTTGCTGAATGCGTGGGGATATGGCGCGCAGAACAAAGCGGAGAGATCCCGGTATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cctgtttggtttagatgttgcccaagccgttaccagggcaccgtgcttctgtgctggt
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es 422;
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                                                                                                                                                                                                  VNPSDYDYTKHDEDSSETSKDNEDK"
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11350. .12099
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IPSIMVQGNSVSVSLAETFSFNKIYAGIGIAFLIGLVVIGGVKRIGKVTEFVVPLMAG
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GSLYIVVYGLSFLHSKIDPRAMYTPTGMFSVVCGFWFFLNTNQLIDFNRIKPIINVVI
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                                                                                                                                                                                                                                                                                                                       VVIVIPALWLMHRLMKKHQDKNIYELLSDSSPIAGRIIILLFSLYFLLINAHDIRFFI
NLINILFLPRTPMAVLGGVIIFVAICIAREGKETLTRMAQIFLFPFGILVLFLPFFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAGMGTAPIAHAAAMTDHPVRQGFWSVIGIVIDTLIICTTTAFIVLASGVWTGKNASN
DPAALTTAAFQHYFGSGGGYFVSVSLVFFVVSTIMVVIFYGVKQAEFLFGRLAGHVIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'translation = "MMDFSHIVSEDKIKRAIKDGDFQNLPGMGKPLPKMTRHTCRNRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'translation="MREKVAKNAVESTFRFDITKCKTRYLSRNKGIKWYIENCMIKYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLLPLLIYLIIKSKALFGAKAKH" complement(5650. .7065)
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complement(7149. .7175)
complement(7190. .7450)
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complement(7582, 7596)
complement(7600, 7737)
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terminator
CDS
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RBS RBS CDS

RBS RBS CDS

2,

Search completed: March 22, 2002, 08:49:30 Job time: 7679 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

· protein search, using sw model OM protein Run on:

US-09-604-231-2 2363 1 MAMVEPSLVNGYDVAATWAA.....IEAGANLLNVAKKBAVPATP 468 Perfect score: Sequence:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

219241 hits satisfying chosen parameters: oţ Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\*
pir2:\*
pir3:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	phosphotransferase	phosphotransferase	scrA protein - Sta	PTS system, beta-g		sphotrans	PTS system, sucros	beta-glucoside per		hypothetical prote	beta-glucoside-spe	hypothetical prote	phosphotransferase	PTS system, trehal	phosphotransferase	phosphotransferase	PTS system, sucros	phosphotransferase	sac operon regulat	levansucrase synth	phosphotransferase	phosphotransferase	PTS system enzyme	PTS system, sucros		PTS system, trehal	phosphotransferase	phosphotransferase	, hypothetical prote
SUMMARIES	ID	S44257	B32243	839978	нв3686	C83724	868599	F82432	140406	JQ0781	T47097	B42603	D86807	C69725	н83926	C25977	S62331	н83881	WQEBST	139868	JU0293	A39938	C65236	A86122	F84096	S46953	B82263	WQBSGS	S18607	D86766
	DB.	~		~	~	~	~	~	~	~	7	7	~	7	~	N	~	~	-	N	~	ď	~	7	~	Н	7	-	Н	7
	Length	651	664	480	630	636	632	479	609	479	609	631	989	470	470	625	456	458	455	372	459	460	473	473	453	692	478	669	651	195
œ	Query	44.8	40.4	29.7	29.4	28.5	28.5	27.9	27.8	27.3	27.3	27.1	24.9	24.1	24.1	24.0	20.7	20.6	20.0	19.8	17.2	16.5	15.5	15.2	14.5	14.5	14.3	13.6	٠.	13.3
	Score	1058.5	953.5	701	695.5	673.5	673	629	657	646	645	640	588.5	570	569.5	567.5	489	487	473	467	406	390	367	360	342.5	341.5	339	321.5	317.5	314
	Result No.	1	7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

PTS system, glucos	phosphotransferase	PTS system, glucos	pnosphotransterase
phosphotransferase	hypothetical prote	phosphotransferase	lactose transport
hypothetical prote	sucrose phosphotra	hypothetical prote	probable PTS enzym
phosphotransferase	hypothetical prote	phosphotransferase	hypothetical prote
D83755	D69750	C83839	H69940
WQEC2N	C86678	G65051	A32241
E85567	B69744	B85920	G85885
S46952	C86766	F70169	D65017
2424	0000	00000	7000
675	631	173	108
648	521	485	634
648	446	485	474
675	454	189	474
12.9 12.6 12.6 12.3	12.2 12.1 12.0 11.9	11.5 11.4 10.8	10.8 10.7 10.7
305.5	287.5	271.5	254.5
298.5	285	270.5	253.5
297.5	283.5	265.5	253.5
289.5	281	256	250.5
30 32 33	34 35 37	8 8 4 4 4 4 9 8 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 5 4 4 3 5

## ALIGNMENTS



phosphotransferase system enzyme II (BC 2.7.1.69), sucrose specific - Pediococcus pen C; Species: Pediococcus pentosaceus
C; Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999
C; Accession: \$44257
R; Leenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
R; Leenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G.
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C; Genetics:
A; Genetics:
A; Genetics:
C; Genetics: Scraft Companies of the component of

ŝ Gaps 23; Length 651; 44.8%; Score 1058.5; DB 2; Length 46.7%; Pred. No. 1.4e-65; Live 78; Mismatches 151; Indels Matches 221; Conservative Best Local Similarity Query Match

1 MAMYFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60 g ò

61 KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120 313 | :|| || || || :::|||||| :|| :|| || || :|| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| ò g

121 VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176 ŏ

g 236 177 KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF g ò

237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE δ qq

297 AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV ò

487 -----INVNDEIISAPVTGASESLKQVNDQVFSAEIMGKGAAIVPSSDQVVAPADGVIT

g

416 357 VAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDI ò

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YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
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A; Title: Cloning and characterization of the Reference number: S39976; MUID:94049686
A; Accession: S39978
Brueckner, R.
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Goetz, F.;
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Matches 152; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | | : | : | : | | | 489 VEEAIEEVQ-EIPEEAASAANKAQVTDEVLAAPLAGEAVELTSVNDPVFSSEAMGKGIAI
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                        DAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL - - LNVAKKEAVPAT
                                                    Indels
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C;Accession: H83686
R;Takami, H: Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Tetle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20263314
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A, Residues: 1-630 <STO>
A, Cross-references: GB.APO01508; GB:BA000004; NID:g10172890; PIDN:BAB04015.1; GSPDB:G
A, Experimental source: strain C-125
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
the scrA gene encoding the sucrose-specific
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                                                                                                                                                                                                     ΙI
                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <WAG>>
A;Cross-references: EMBL:X69800; NID:9407905; PIDN:CAA49461.1; PID:9407908
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
                                                                                                                                                                                                                                                                                                                                                                                                                                      HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK-SE 174
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Best Local Similarity 51.4%; Pred. No. 4.7e-41;
Matches 146; Conservative 49; Mismatches 81;
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A)Gene: scrA
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
C;Keywords: phosphotransferase; sugar transport system
F;480-632/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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    Streptococcus

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F82432
P192432
P192432
P192432
P1925 Specific IIBC component VCA0653 [imported] - Vibrio cho.
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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                                                           GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK
                                                                                                                                                                                                                                          phosphotransferase system enzyme II (EC 2.7.1.69), sucrose-specific NAlternate names: sucrose-specific enzyme II C; Species: Streptococcus sobrinus A; Variety: strain 6715 C; Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-M C; Accession: $68599 F; Chen, Y.Y.M.; Lee, L.N.; Lealanc, D.J. Infect. Immun. 61, 2602-2610, 1993 A; Title: Sequence analysis of scrA and scrB from Streptococcus sobril A; Reference number: $68598; MUID:93273516 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-632 < CHE>
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                                                                                                                                                                                                                                             (EC 2.7.1.69), sucrose-specific enzyme II
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C;Genetics:
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizci, A.; Galicch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Sano, A, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sakowska, A.; Seanla, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Reference. number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: bglP
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
F;458-609/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-287, FF', 289-433, 'G', 435,'S', 437-448,'HR', 451-548,'M',550-551,'S',553-60 A;Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB15963.1; PID:926364 A;Experimental source: strain 168
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Best Local
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C.Species: 14040, S65814, 669594; 847174
R.Le Coq, D.; Lindmer, C.; Kruger, S.; Steinmetz, M.; Stulke, J.
J. Bacteriol. 177, 1527-1535, 1995
A; Fitle: New beta-clucoside (bgl) genes in Bacillus subtilis: the bglP gene product has A; Reference number: 140404; MUID:95189730
A; Fitle: New beta-clucoside (bgl) genes in Bacillus subtilis: the bglP gene product has A; Residues: 140406
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-609 <-RES>
A; Cross-references: EMBL:234526; NID:9505573; PIDN:CA884286.1; PID:9505576
R; Beloin, C.; Hirschbeln, L.; Le Hegarat, F.
Mol. Genet. 250, 761-766, 1996
A; Fitle: Suppression of the Bgl+ phenotype of a Delta-hns strain of Escherichia coli by A; Reference number: S6579; MUID:96204517
A; Accession: S65581
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-74, S', 76-182 <-BEL.
A; Residues: 1-74, S', 76-182 <-BEL.
A; Cross-references: EMBL:885408; NID:91037169; PIDN:CAA59697.1; PID:91037172
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
B; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; Ch.; Bruschi, C., Ferrari, E., Brianch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E., Branchich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E., Branchich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.,
C; Accession: F82432
R; Heidelberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
A; Accession: F82432
A; Molecule type: DNA
A; Residues: 1-479 <HEI>A; GspbB:GNO1
A; Strain N16961; biotype El Tor
C; Genetics: Residues: 2
A; Superimental source: serogroup Ol; strain N16961; biotype El Tor
C; Genetics: A; Map position: 2
C; Superimanly: phosphotransferase system sucrose-specific enzyme II, factor II
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beta-glucoside permease - Bacillus subtilis
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A;Molecule type: DNA
A;Residues: 1-631 <EL1>
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:Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
A;Status: preliminary
A;Molecule (type: DDA)
A;Residues: 1.479 cBLA>
A;Residues: 1.479 cBLA>
A;Residues: 1.479 cBLA>
A;Cross-references: GB:M76768; GB:M30194; NID:g155261; PIDN:AAA27555.1; PID:g155262
C;Genetics:
A;Genetics:
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein N17C [imported] - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C;Accession: T47097
R;Yoshida, K.; Sano, H.; Seki, S.; Oda, M.; Fujimura, M.; Fujita, Y.
M;Crobiology 141, 337-343, 1995
A;Title: Cloning and sequencing of a 29 kb region of the Bacillus subtilis genom A;Reference number: 224350; MUD:95219088
A;Accession: T47097
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Hostule: preliminary; translated from GB/EMBL/DDBJ
A;Hostules: 1-609 < vgos.
A;Fesidues: 1-609 < vgos.
A;Fesidues: 1-609 < vgos.
A;Cross references: EMBL:D31856; NID:g603765; PIDN:BAA06652.1; PID:g603778
A;Experimental source: strain BGSCIAl
C;Geneling: A;Gene: NI7C
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                        KRLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                           VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                                                                                                                                                                                                                                           PVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQ 132
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                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                    MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH,60
                                                                                                                                                                                                                                                                                                                                                                                                                             KGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPPPIELELFNQGG-SFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                      9
                                                                                                                                                   Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 609;
                                                                                                                                                 Ouery Match 27.3%; Score 646; DB 2; Length 47 Best Local Similarity 46.5%; Pred. No. 2.9e-37; Matches 128; Conservative 54; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 645; DB 2; Length 60 ilarity 33.6%; Pred. No. 4.5e-37; Conservative 86; Mismatches 178; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 LGVVSIDAPDMVMFLVCA-VVTFFIAFGAAIAYGL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::|| || |: : : |: | || |: |: || PGIISI-TPDKIGYYIAGMVIAFLTAFVLTIVLGI 467
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Best Local Similarity
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Best Local Simi
Matches 154;
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A;Gene: arbr
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
F;479-631/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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C; Species: Erwinia chrysanthemi
C; Date: 04 Sep-1998 #sequence_revision 04 Sep-1998 #text_change 16-Jul-1999
C; Accession: B42603
B; El Hassouni, M.; Henrissat, B.; Chippaux, M.; Barras, F.
J. Bacteriol. 174, 765-777, 1992
A; Title: Nucleotide sequences of the arb genes, which control beta-glucoside utilizat olase family including enzymes from eubacteria, archeabacteria, and humans.
A; Reference number: A42603; MUID:921211114
A; Accession: B42603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B42603
beta-glucoside-specific phosphotransferase system-dependent permease - Erwinia chrysa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVY 122
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TEPAMYGVNMRLKKPFAAALIGGAAGGAFYGMTGVASYIVGGNAGLPSIPVFIGPTFIYA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M81772; NID:g148385; PIDN:AAA24814.1; PID:g148387 A;Note: sequence extracted from NCBI backbone (NCBIN:77835, NCBIP:77537) C;Genetics:
                                                                                                                                                                                                                                                  182 ASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTII
                                                                                                                                                                                                                 311 QAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTK
                                                                                                                                                                                                                                                                                                                                                     AEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVCVIFGLHWGFVPLMLNNFSVIGHDTLLPLLVPAVLGQAGATLGVLLRTQDLKRKGIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 IDAPDMVMFLV-CAVVTFFIAFG-AAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAI
                                                                                                                                       MIGLVIAF -- AAGTSAAYLL -----GFED -----VPS ----HRSQQPAVHEGSREII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 VVSNYKK--TGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
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Naturbors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallatthors: Roulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hullo, M. Koetter, P.; Koningstein, G.; Kenatt, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Fuch, H.; Masuda, S.; Maulo, Y., M.; Ogwar, K.; Ogivara, A.; Odudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl, M.; Bivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl, A, Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sea akeuchi, M.; Tamanokoshi, A.; Tomanoto, H.; Yamane, K.; Yasumoto, V.; Odolya T.; Winters, P.; Wipat, A.; Tananoto, H.; Yamane, K.; Yasumoto, V.; Osohida A, Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Authors: Schikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Authors: Sonic Gogyzs
A.Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Accession: Gogyzs
A.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.; Rocellues: 1-470 ckUN>
A.; Accession: Gogyzs
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A.; Rocellues: 1-470 ck
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A,Residues: 1-139,'S',141-362,'L',364-464,'G',466-470 <SC2>
A;Cross-references: EMBL:254245; NID:g1000450; PIDN:CA91014.1; PID:g1000451
C;Comment: This enzyme functions as the specific trehalose transporter. It belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPIVITGLHQSFPPIELELFNQ--GGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
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C; Superfamily: phosphotransferase; sugar transport system
C; Keywords: phosphotransferase; sugar transport system
C; Keywords: phosphotransferase; sugar transport system
F; 118-131/Domain: transmembrane #status predicted <TM2>
F; 160-181/Domain: transmembrane #status predicted <TM3>
F; 230-245/Domain: transmembrane #status predicted <TM5>
F; 363-286/Domain: transmembrane #status predicted <TM6>
F; 375-355/Domain: transmembrane #status predicted <TM6>
F; 375-395/Domain: transmembrane #status predicted <TM6>
F; 375-395/Domain: transmembrane #status predicted <TM6>
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Rybolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. in press, 2001
Ryference number: A86625
Rycession: D86807
Rycession: D868
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C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C; Accession: C69725; S67929; JC5037; 140497; S67864
R; Kunst, F; Ogasawara, N: Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd C.; Broillet, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ptbA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C.Species: Lactococcus lactis subsp. lactis C.Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
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Job time: 152 sec
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Best Local Similarity 30.8%
Matches 142; Conservative
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                                                                                                                                                            C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Accession: H83226
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Accession: H8326
A;Status: preliminary
A;Molecule type: DNA
A;References: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05935.1; GSPDB:GNOC
A;Experimental source: strain C-125
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
                                                                                                                                               trehalose-specific enzyme II, BC component BH2216 [imported] - Bacillus halo
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Status: preliminary
Molecule type: DNA
Molecule type: Molecule type:

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Gaps

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Sequence 5658, Ap
Sequence 5658, Ap
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5: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/USO0_NEW_COMB.pep:*
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-897-516-6783
PCT-US-0398-5558
US-09-815-242-5658
US-10-072-881-5658
PCT-US-0398-12270
US-09-815-242-12270
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Gapop 10.0 , Gapext 0.5
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sedneuce 12942, 1	Sequence 10089, 1	Sequence 10089, 1	Sequence 10089, 1	Sequence 10500, 1	Seguence 10500, 1	Sequence 10500, 1	Sequence 5660, Ap	Sequence 5660, Ap	Sequence 5660, Ap	Sequence 10243, /	Seguence 10243, 1	Seguence 10243, 1	Sequence 6596, Ap	Sequence 7609, Ap	Sequence 12479, 1	Sequence 12479, 1	Sequence 12479, 1	Sequence 11950, 1	Sequence 11950,
Sedn	Sedn	Sedu	Sedu	Sedu	Sedu	Sedu	Sedn	Sedu	Sedu	Sedn	Sedu	Sedu	Sedn	Sedu	Sedu	Sedu	Sedu	Sedn	Sedn
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300	298.5	298.5	298.5	292	292	292	288.5	288.5	288.5	250.5	250.5	250.5	247.5	233.5	229	229	229	226.5	226.5
92	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 13467, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
FILE REFERENCE: ELITRA.028VPC
CURRENT PAPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR PLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-03
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8.1e-41;
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                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4:0
                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptococcus pneumoniae PCT-US02-03987-13467
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PCT-US02-03987-13467
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LENGTH: 627
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                       418 AIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
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FILE NEERENCE: ELITEA, 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOM APPLICATION NUMBER: 60/191,078
PRIOM APPLICATION NUMBER: 60/206,848
PRIOM PELING DATE: 2000-05-23
PRIOM FILING DATE: 2000-05-23
PRIOM PAPLICATION NUMBER: 60/207,727
PRIOM PAPLICATION NUMBER: 60/207,727
PRIOM PAPLICATION NUMBER: 60/242,578
PRIOM PAPLICATION NUMBER: 60/242,578
PRIOM APPLICATION NUMBER: 60/253,625
PRIOM APPLICATION NUMBER: 60/257,931
PRIOM FILING DATE: 2000-11-27
PRIOM PAPLICATION NUMBER: 60/257,931
PRIOM PRILING DATE: 2000-12-22
PRIOM APPLICATION NUMBER: 60/257,931
PRIOM PAPLICATION NUMBER: 60/257,931
PRIOM PAPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13467
                                                                                                                                                                                       ; Sequence 13467, Application US/09815242; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Zyskind, Judith W.
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Best Local Simi
Matches 159;
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APPLICANT:
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APPLICANT:
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APPLICANT: Bussey, Howard TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Proliferation
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                                                                                                    AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                     -APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KRLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 MLYVGNGQLPQYLLMVAVSFALGFALTYMFGY-----EDEVDATAAAKQAEVAEEKEE 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 MMLVSGSLPNAWAVA---QGGEVTAMNFFGF-IPVVGLQGSVLPAFIIGVVGAKFEKAVR 237
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                             VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAE
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                                                                                                                                                                                                         418 AIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                    Query Match 27.9%; Score 660; DB 7; L
Best Local Similarity 34.3%; Pred. No. 8.1e-41;
Matches 159; Conservative 92; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICAMP.
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PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptococcus pneumoniae US-10-072-851-13467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck, Robert
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
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Roemer, Terry
Jiang, Bo
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AVALG---AAGFLGVVSIDA-PDMVMF----LVCAVVTFFI-------260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 TKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTT 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 LTFIAIGPAMRWVGDVLAHGLQ----GLYDFGGPVGGLLFGLVYSPIVITGLHQSF---- 134
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION UMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Mismatches 192;
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                                                                                                                                                                                                                                                                                                                                                                                   14.6%; Score 345.5; 24.2%; Pred. No. 1.4
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5658
LENGTH: 679
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                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.0280PC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Harsomil-Osterfeld, Karina C.
APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Splridonov, Sergel
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US(09/987,516
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAVFFLAKSEKLK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL 237
                                                                                                           AFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDID 417
                                                                                                                                                  1 MAMVFPSLVNGYDVAATMAAGEMP-MWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 16.8%; Score 396; DB 6; Length 47 Best Local Similarity 31.5%; Pred. No. 1.6e-21; Matches 88; Conservative 70; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                      418 AIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6783, Application US/09897516 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-6783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US02-03987-5658
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US-09-897-516-6783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 WFEFGSWKNAAGEIIHGDQRIFIEQIREGAHLTAGKFMQGEFPVMMFGLPAAALAIYHSA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFL----ITPVLTLLTGF 82
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                                                                                                                                                                                                                                                                                                                                                                                                                            192;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.6%; Score 345.5; DB 6
Best Local Similarity 24.2%; Pred. No. 1.4e-17;
Matches 132; Conservative 68; Mismatches 192
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
        PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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GENERAL INFORMATION:
APPLICANT: Carr, Grant J.
APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus
US-09-815-242-5658
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648 PIIVT 652
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APPLICANT: BUSSEY, HOWARD
TITLE OF INVENTION: Methods for identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Methods for identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER: OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------RNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 345.5; DB 7; 24.2%; Pred. No. 1.4e-17; ive 68; Mismatches 192;
Foulkes, J. Gordon
Zamudio, Carlos
Haselbeck, Robert
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
Jiang, Be
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US-10-072-851-5658
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648 PIIVT 652
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593 ---VSDSGLELLIHIGEDTVKLNGEGFTLHVEEGOEVKOGDLLINFDLDVIRNHAKSDIT 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 LTFIAIGPAMRWYGDVLAHGLQ----GLYDFGGPVGGLLFGLVYSPIVITGLHQSF---- 134
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                                                                                                          Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 345.5; DB (
Pred. No. 1.4e-17
                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                              CURRENT PELICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-28
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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24.2%;
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Best Local Similarity
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LENGTH: 681
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                                                                          APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 SILGIPTLOTGVFGGIIIGALAAW---CYNKFYNINLPSYLGFFAGKRFVPIM-MATTSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I -- LAFPMALIW -- PTIQTGLNAFSTGLLDSNTGVAVFLFGFIKRLLIPFGLHHIFHAPF 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.6%; Score 345.5; DB 1; Best Local Similarity 24.2%; Pred. No. 1.4e-17; Matches 132; Conservative 68; Mismatches 192;
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                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12270
LENGTH: 681
                                    Sequence 12270, Application PC/TUS0203987 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Staphylococcus aureus
PCT-US02-03987-12270
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PIIVT 654
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Gaps

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APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
TITLE OF INVENTION: Proliferation
CURRENT PELITRA, 0.28 VPC
CURRENT APPLICATION NUMBER: PCT/USO2/03987
CURRENT FILING DATE: 2002-02-02
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10809
369 TKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTT 428
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA 011A
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                                                                                                                                                                                                                                                             Sequence 10809, Application PC/TUS0203987 GENERAL INFORMATION:
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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PCT-US02-03987-10809
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Best Local Simi
Matches 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastEED for Windows Version 4.0
                                                                                                                                             Sequence 12270, Application US/10072851 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Id
TITLE OF INVENTION: Proliferation
                                                                                                                                                                              APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-072-851-12270
                                                                                                                                                                                                                                                                                                              Wall, Daniel
Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
Jiang, Bo
Boone, Charles
             429 PIVVS 433
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10-072-851-12270
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APPLICANT: Goldman, Barry S.
APPLICANT: Hubsing, Joseph E.
APPLICANT: Hubsing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Steven C.
APPLICANT: Solitionov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences and Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR PILING DATE: 2000-06-30
SEQ ID NOS: 8409
SEQ ID NOS: 8409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 EKQLHKIVPESIDIIVTPTISLLVIGLATIFLIMP----VAGAISNGLVGIINVVLEKGG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 PVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG-SFIFATASMANIAQGAACLAVFFL 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 EKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDF----GG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 338.5; DB 7; Length 33.2%; Pred. No. 2.9e-17; Live 54; Mismatches 114; Indels
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10809
LENGTH: 484
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                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecalis
US-10-072-851-10809
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Best Local Similarity 33.2%
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Best Local Similarity
Matches 77; Conserv
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APPLICANT: Boone, Charles
APPLICANT: Boone, Charles
TITLE OF INVENTION: Howard
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITHA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%; Score 338.5; DB 6; 33.2%; Pred. No. 2.9e-17; Live 54; Mismatches 114;
                                CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-12-3
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASTSEQ FOR WINGOWS VERSION 4.0
SED ID NO 10809
        CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
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GENERAL INFORMATION:
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Yamanicli Daniel
APPLICANT: Yamanick, John D.
APPLICANT: Yamanick, Robert T.
APPLICANT: Roemer, Terry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecalis
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Best Local Similarity 33.2%
Matches 94; Conservative
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Sequence 12272, Application PC/TUS0203987

SEGUENCE 12272, Application PC/TUS0203987

GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits of TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.02894PC
CURRENT APPLICATION NUMBER: PCT/US02/03987

CURRENT FILING DATE: 2002-02-02

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 15811

SOFTWARE: RastsEQ for Windows Version 4.0

SEQ ID NO 12272

LENGTH: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                            GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 FLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVIT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLAKSEKL--KGLAGASGV 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
PCT-US02-03987-12272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.79
Best Local Similarity 32.29
Matches 96; Conservative
                                                                                                                                                                                                                                   RESULT 15
PCT-US02-03987-12272
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418 NI 419
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Search completed: March 21, 2002, 16:27:36 Job time: 337 sec

Sequence 21, Appl Sequence 16, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Patent No. 5254799

Sequence 7, Appli Patent No. 552311 Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 10, Appli

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
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PAPLICATION NUMBER: US/07/828,788A
FILING DATE: 19920129
CLASSIFICATION: 435
                                                                                                                                                                                                             US-08-836-325-7
5523211-1
US-08-810-720-13
US-08-46-7
US-08-46-7
US-08-157-363A-10
US-08-463-308-6
US-09-231-818-21
US-08-86-325-16
US-08-678-039A-40
US-08-960-048-10
US-09-120-513-2
US-09-450-105-2
5254799-7
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PCT-US93-11405-10
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2421 N.W. 41st STREET, SUITE A-1
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ZIP: 32606
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/07828788A Patent No. 5273746
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NAME: SALIWANCHIK, DAVID R.
REGIGSTRATION NUMBER: 31,794
REFERENCE/CDCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
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IMMEDIATE SOURCE:
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CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE
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STREET: 24
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US-07-828-788A-12
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488.023 Million cell updates/sec
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Sequence 12, Appli
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Patent No. 5164180
Patent No. 5188960
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Sequence 2, Appli
Sequence 2, Appli
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                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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DCT-US22-11337-12
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US-08-911-364-1
US-08-464-700-2
US-08-836-325-2
US-08-836-325-12
US-08-836-325-12
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-08-510-646B-22
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-08-814-877-4
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                     13;
                                                                                                                                                                                                      ---AEFSN----DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 336
                                                                                                                                                                                                                                                          337 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 396
                                                                                                                                                                                                                                                                                           494 DILRITSPGOISTL---RVTITAPLSQRYRVRIRY--ASTINLOFHTSIDGRPINGGNFS 548
                                                                                                                                                                                                                                                                                                                                397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                     549 ATMSSGGULQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 593
                                                                     Gaps
                                  Length 1176;
                                                                     Indels
                                                                                                        249 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG--
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,034
                               ; Score 113.5; DB 1;
; Pred. No. 0.019;
43; Mismatches 96;
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/210,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/865,168
FILING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
CLASSIFICATION: 435
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APPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08356034
Patent No. 5691308
GENERAL INFORMATION:
APPLICANT: PAYRE, Jewel M.
                                 4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Saliwanchik, Roman REGISTRATION NUMBER: 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                295 AEA-----EAP----
                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 : : | |||
594 YIERIEFVPA 603
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                                                                   26;
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COUNTRY:
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US-08-356-034-2
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Matches
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Sequence 2, Application US/08933891
Patent No. 6096708
PATENT No. 6096708
APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding TITLE OF INVENTION: No. 6096708el Lepidopteran Pests, and Genes Encoding TITLE OF INVENTION: No. 6096708el Lepidopteran-Active Toxins NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 AEA-----EAP----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.8%; Score 113.5; DB 1;
22.4%; Pred. No. 0.019;
11ve 43; Mismatches 96;
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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                                                                                                                                                                                                                                                               BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                      STRAIN: AIZAWAI.
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
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(904)372-5800
                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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594 YIERIEFVPA 603
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Best Local Similarity
Matches 56; Conserv
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494 DILRITSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 LFVLDGTEFSFASLTADLPSTIY -- RQRGTVDSLDVIPPQDNSVPARAGFSHRLSHVTML 434
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INMEDIATE SOURCE: LIBRARY OF AUGUST SICK CLONE: 811A2
                                                                                                                                         COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US92/11337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904,375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 97/828,788
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US-08-040-751-1
Sequence 1, Application US/08040751
; Patent No. 5407825
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FILING DATE: 19921231
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STRANDEDNESS: single
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                              STREET: 2421
CITY: GAINESVILLE
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594 YIERIEFVPA 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : :: || : : | : : | : : | : : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : | . : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8%; Score 113.5; DB 3; Length 1176; 22.4%; Pred. No. 0.019; tive 43; Mismatches 96; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application PC/TUS9211337
GENERAL INFORMATION:
APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF ENVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MA43.C1.D1
                                                                    APPLICATION NUMBER: US/08/210,110 FILING DATE: APPLICATION NUMBER: 07/865,168
                                                                                                                                                                        PILING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/311,955
FILING DATE: 27-JUN-89
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
REGISTRATION NUMBER: 21,023
REFERRENCE/DOCKET NUMBER: 21,023
REFERRENCE/DOCKET NUMBER: MA43.C1.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (904)372-5800
INFORMATION FOR SEQ ID NO: 2:
ERQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
   APPLICATION NUMBER: US/08/356,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: BACILLUS THURINGIENSIS
                                                                                                                                             JMBER: 07/865,168
09-APR-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 ATMSSGGNLQSG---
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Best Local Similarity
Matches 56; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457 NVAKKEAVPA 466
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594 YIERIEFVPA 603
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108 AGVKPGKVPGVGLPGV-----YPGGVLP------GARFPGVG------ 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 TTGKLP-YGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKFGAGAAGVLPGVGGA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL---- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GVPGVPGAI-PGIGGI-----AGVGTPAAAAAAAAA--AKAAKYGAAAGLVPGGP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ---VCAVVTFFIAFGAAIAYGLYLVRRNG---------SIDPDATAAP-- 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GVVSIDAPDMVMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 195;
                                                                                                                        APPLICANT: RCTHSTEIN, Aser
APPLICANT: REELY, Fred W.
APPLICANT: RCHESTEIN, Steven J.
APPLICANT: ROTHSTEIN, Steven J.
TITLE OF INVENTION: SELF-ALIGNING PEPTIDES MODELED ON HUMAN
TITLE OF INVENTION: ELASTIN AND OTHER FIBROUS PROTEINS
NUMBER OF SEQUENCES: 8
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 731;
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,364
FILING DATE: 07-AUG-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 108.5; DB 2;
; Pred. No. 0.03;
47; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bent, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 041082/0104
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,552
FILING DATE: 07-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                               ; Sequence 1, Application US/08911364
; Patent No. 5969106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 20.68
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-911-364-1
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                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 20007-5109
                                                                                                         GENERAL INFORMATION:
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                                         US-08-911-364-1
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                 APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. 54078
TITLE OF INVENTION: Lepidopteran-active Toxins
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 LFVLDGTEFSFASLTADLPSTIY--RQRGTVDSLDVIPPQDNSVPARAGFSHRLSHVTML 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4:8%; Score 113.5; DB 1; Length 1179; 22.4%; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK CLONE: 81RR1
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .96
                                                                                                                                                                 ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
CITY: GAINESVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE/DOCKET NUMBER: MA39.C1.D3
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPEAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                        32606
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Matches 5
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APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                            303
                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                        364 GVGVGGIPTYGVGAGGFPGFGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 ------VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASG-KLGSGV 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 GVAPGVG--VAPGIG-----PGGVAAAAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGV 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 NG------LCEFD 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      536 PGLGVGGGVPGLGVGGCPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGA 595
                                                                            ---GARFPGVG------ 140
                                                                                                                        76 TLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL-VYSPIVITGLHQSF 134
                                                                                                                                                                                                                  135 PPIELELFNOGGSFIFATASMANIAOG------AACLAVFFLAKSEKLKGLAGA 182
                             16 ATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVL 75
                                                                                                                                                                                                                                                          198 TTGKLP-YGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAAAKFGAGAAGVLPGVGGA
                                                                                                                                                                    141 --VLPGVPTGAGVKPKAPGVGGAFA-GIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPY
                                                                                                                                                                                                                                                                                                                                                            257 -GVPGVPGAI-PGIGGI-----AGVGTPAAAAAAAA--AKAAKYGAAAGLVPGGP
                                                                                                                                                                                                                                                                                                                                                                                                          .....GVVSIDAPDMVMFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------SIDPDATAAP--
                                                                                                                                                                                                                                                                                                                183 SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 IDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KESSLER, GOLDSTEIN & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 ---VCAVVTFFIAFGAAIAYGLYLVRRNG-------
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                                                             110 AGVKPGKVPGVGLPGV-----YPGGVLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
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1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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US-08-836-325-2
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                                                                                                                                                                                                 362 GVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGVPGVGGVPGVGISPEAQAAAAA 421
                                                                    -----VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASG-KLGSGV 338
                                                                                                                   422 KAAKYGVGTPAAAAAKAAAKAAQFGLVPGVGVAPGVGVAPGVGVAPGVGLAPGVGVAPGV 481
                                                                                                                                                                 339 AIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDT-----VNL 390
                                                                                                                                                                                                                                                                 -----THFNPLKKQGDEVKAGEL-----LCEFD 415
                                                                                                                                                                                                                                                                                                           534 PGLGVGAGVPGLGVGAGVPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGA 593
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,700
FILING DATE: 7-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.6%; Score 108.5; DB 4; Best Local Similarity 20.6%; Pred. No. 0.03; Matches 122; Conservative 47; Mismatches 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6232458
GENERAL INPRMATION:
APPLICANT: WEISS, ANTHONY S
APPLICANT: MARTIN, STEPHEN L
TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 7-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL6520
FILING DATE: 22-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL9661
FILING DATE: 28-JUN-1993
APPLICATION NUMBER: PCT/AU93/00655
FILING DATE: 16-DEC-1993
ATORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: GHC3!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08464700
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 733 amino acids
amino acid
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TELEPHONE: 215-540-5818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19477
COMPUTER READABLE FORM:
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US-08-464-700-2
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STATE:
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TITLE OF INVENTION: The NUMBER OF SEQUENCES: 19 CORRESPONDENCE ADDRESS:
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                                                                                                  Washington
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                                                             ADDRESSEE:
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                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                      COUNTRY:
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                                                                                 STREET:
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Best Local Si
Matches 91;
                                                                                                  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 FLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPYGGLLFGLVYSPIVITGLHQSFPPIELEL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 RLRWPFFI----GIGTAA------IGGALIALFNIKAVALGAAGFLGVVS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 LLFLVMFIYAIFGMSNFAYVKKEAGINDMFNFETFGNSMICLFQITTSA-GWDGLLAPIL 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 IDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAMFASGKLGSGV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             810 VATEESTEPLSEDDFEMFYEVWEKFDPDAT------QFIEFCKLSD--FAAALDPPLL 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        860 IAKPNKVOLIAMDLPMVSGDRIHCLDILFAFTKRVLGE-GGEMDSLRSOMEERFMSANPS 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 FNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 AIVPIKGQLVS----PVSGKIVVAFPSGHAFAVRTKAEDGSNVDIL----MHIGFDTVNLN 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 LFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFL-----ITPVLTLLLTG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 108; DB 3; Length 1011;
20.7%; Pred. No. 0.055;
Live 67; Mismatches 168; Indels 114;
                                                                                                                                                                                                               0917.0240002
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
                                                         08/482,401
                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | ||:::|| || || || || || 919 KVSYEPITTTLKRKQEEVSA 938
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                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                 APPLICATION NUMBER: 08/48 PTT.TNG DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                            1011 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91; Conservative
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                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                              LENGTH:
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1602 Y-----FVSPTLFRVIRLARIGRILRL----IKGAKGIRTLLFALMMSLPALFNIGL 1649
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                                                                           GOLDSTEIN & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
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Mismatches 168;
                                                                                                    N. W., Suite 600
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Similarity 20.7%; Pred. No. 0
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APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR PAPLICATION NUMBER: 08/482,401
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                         3: STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,203
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: not relevant not relevant
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Thereof
                                                                                                                                                                                                  ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1989 amino acids
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1597 IEK----YFVSPTLFRVIRLARIGRILRL-----IKGAKGIRTLLFALMMSLPALFNIGL 1647
                                                                                                                                                                                                                                                  1707 NSAPPDCDPKKVHPGSSVEGDCGNPSVGIFYFVSYIIISFLVVVNMYIA----VILENFS 1762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 IDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGV 338
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                                                                     142 FNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNL
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TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,860
FILING DATE: 18-MAY-1989
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Best Local Similarity 22.47
Matches 56; Conservative
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597 YIDRIEFVPA 606
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5164180-6
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5188960-2
;Patent No. 5188960
   1559 ECVLKLIS-
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5164180-6
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
82 FLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.5%; Score 107; DB 3; L. Best Local Similarity 20.7%; Pred. No. 0.2; Matches 91; Conservative 66; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX I
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0917.0240002
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APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
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FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
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APPLICATION NUMBER: 08/482,401
FILING DATE: 07-UNN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08836325 Patent No. 6110672
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1874 KVSYEPITTIKRKQEEVSA 1893
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                               392 GTHFNP----LKKQGDEVKA 407
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COMPUTER READABLE FORM:
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US-08-836-325-10
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Length 1864;

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62 RL-------KGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQG 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 VSSFGA-----SGTNAHVVLESVPAGEPPAAGRPEDTGGAW---TVS----GRGPAAL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 AVFFLAKŠEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI---A 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 RAQAARLYDALTGTGTGTGTGQGAGQG-------AGPGTAEVAGALAHART 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 LFNIKAVALGA-----AGFLGVVSIDAPDMVMFLVCAVV----TFFIAFG-----AAIA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 YGLYLVRRN------GSIDPD-----ATAAPVPAGTTKAEAEAPAEFSN 305
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                                                                                                                                                                                                                                                                                                                                                             ; Score 106.5; DB 2;
; Pred. No. 0.2;
45; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: DeWitt Ross & Stevens S.C. STREET: 8000 Excelsior Drive, Suite 401
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,344
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                                                                                                                                                                                                                                                                                                                                                                    4.5%; 21.7%;
                                                                                                                 1864 amino acids
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                                        INFORMATION FOR SEQ ID NO:
                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: protein
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ZIP: 53717-1914
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 94; Conserv
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US-08-801-344-9
                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       552 ATMSSGGULQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 AEA-----EAP----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1179;
; APPLICANT: PAYNE, JEWEL;SICK, AUGUST J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
;AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhatcoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%; Score 106.5; 22.4%; Pred. No. 0.1; iive 42; Mismatches
                                                                                                   | CURENT APPLICATION OF SEQUENCES: 8 | CURRENT APPLICATION DATA: | APPLICATION NUMBER: US/07/451,261 | FILING DATE: 14-DEC-1989 | PRIOR APPLICATION DATA: | APPLICATION NUMBER: 371,955 | FILING DATE: 27-JUN-1989
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FILING DATE: February 21, 1997
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STREET: LILLY CORPORATE CENTER
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NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
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IBM Compatible
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MEDIUM TYPE: Floppy
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Matches 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 LVYS-PIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 KISSKPLMLPNRHK-------MILAALVVSFLLLIVFVRTDSVGLQ- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 LAGASGVSAVLGITEPA-IFGVNLRLRWPFFIGIGTAAIGGA----LIALFN-IKAVALG 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 LGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKA---------EDGSNVDI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | : | : | 342 FG-----IHPVAGRL-----PGHMNVLLAEAKVPYDIVLEMDEINDDFADTDT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 151; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AAGFL-----GVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 462;
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pyridine nucleotide transhydrogenase, subunit ORGANISM: B
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21.1%; Pred. No. 0.029;
ive 66; Mismatches 123;
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APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim E.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF
TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2106
TELEPAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 21.18
Matches 91; Conservative
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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CLASSIFICATION: 435
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60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPVGGLLFG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 TIFGPDTGNVGWILLAMVIGGAIGIRLAKKVEMTEMPELVAILHSFVGLAAVLVGFNSYL 107
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21.1%; Pred. No. 0.029;
Ive 66; Mismatches 123; Indels 151; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pyridine nucleotide transhydrogenase, subunit ORGANISM: B US-09-498-599-9
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                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
CLACCOMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: CLACCOMPUTER: COMPUTER: CLACCOMPUTER: CLAC
8000 Excelsior Drive, Suite 401
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NAME: Sara, Charles S.
REERRENCE/DOCKET NUMBER: 09820.037
TELEPRONCATION INFORMATION:
TELEPHONE: 608-831-2106
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 amino acids
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Best Local Similarity 21.11
Matches 91; Conservative
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                                                                                                                                         COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
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us-09-604-231-2.rai

Search completed: March 21, 2002, 16:23:16 Job time: 147 sec

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166.5
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(without alignments)
814.145 Million cell updates/sec
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2363
1 MAWYFPSLVNGYDVAATMAA.....IEAGANLLNVAKKEAVPATP 468
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                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*

Description	C.glutamicum phosp	C qlutamicum prote	Brevibacterium lac	C.alutamicum phosp	C glutamicum prote	C.glutamicum phosp	Escherichia coli p	C.glutamicum phosp	B. burgdorferi ant	Amino acid sequenc	B. burgdorferi ant
SUMMARIES	AAB66707	AAG92650	AAB69080	AAB66708	AAG93207	AAB66721	AAG98282	AAB66723	AAY20012	AAY53620	AAY20013
	22	22	22	22	22	22	22	22	20	21	20
% Query Match Length DB	468	661	661	362	683	683	648	135	167	583	135
% Query Match	100.0	100.0	98.7	77.1	19.8	19.8	12.6	6.6	6.6	9.6	7.0
Score	2363	2363	2332	1821	468.5	468.5	298.5	234	233.5	232.5	166.5
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standard; protein;	7	
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Phosphoenolpyruvate; sugar		rase system; PTS.
orynebacterium glutamicum		
000WO-1B0097	3.	
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Kroeger B, S	Н, Z	elder O, Haberhauer G;
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	camicum phosphoenolpy coenclpy two acts and a sugar sbacterium glutamicum (02583-A2.  1-2001.  1-2000; 2000WO-IB0097  1-1999; 99US-014269  1-1999; 99DE-104209  1-1999; 90DE-104209	oenolpyruvate protei; sugar phosphotrans tamicum.  -IB009730142691014269101420951042097I B, Schroeder H, r B, Schroeder H, r B, Schroeder B, r B, Schroeder H,

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                                    phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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                               present invention relates to Corynebacteium glutamicum
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              Claim 4; Page 101-102; 144pp; English.
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The present invention provides a number of nucleotide and protein asquences from the Corpreform bacterium Corynebacterium glutamicum. These sequences from the Corpreform bacterium, one of a gene derived from a mutant of coryneform bacterium, measuring expression amount and amalyshing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Senoh A,
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                                                           AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
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                                                                                                                                                                                                   sugar phosphotransferase system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 mamvfptlvngydvaatmtagempmwslfgldvaqagyggtvlpvlvvswilatiekflh 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                     phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system.
                                                                                                                                      Brevibacterium lactofermentum sucrose PTS enzyme II protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents the Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                     lactofermentum; sucrose PTS enzyme II; sucrase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 661;
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Pred. No. 1.6e-224;
                                                                                                                                                                                                                                                                                                                                                                                                                      Kurahashi O;
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                                          AAB69080 standard; Protein; 661
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                                                                                                                                                                                                                                Brevibacterium lactofermentum
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                                                                                                                                                                                                                                                                                                                                                          99JP-0189512
                                                                                                         (first entry)
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Matches 461; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (AJIN ) AJINOMOTO CO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      Sugimoto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-138150/14.
N-PSDB; AAF32543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 AA;
                                                                                                                                                                     Brevibacterium
                                                                                                                                                                                                                                                             WO200102584-A1
                                                                                                                                                                                                                                                                                                                                                        02-JUL-1999;
                                                                                                       20-APR-2001
                                                                                                                                                                                                                                                                                            11-JAN-2001
                                                                        AAB69080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                            sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                                                                                                                                                                                                                        phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microcorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLA 166
Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 362;
                                                                                                                                                                                                                                                                    The present invention relates to Corynebacteium glutamicum
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; Pred. No. 9.6e-174;
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0; Mismatches
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99DE-1042095.
99DE-1042097.
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                                                                                                                                                                                                                                                                                                                                                                                                         262 FGAAIAYGLYLVRRNGSID-
                                                                                                                                                                      Conservative
                                                                           European Patent Office
                                                                                                                                                         Similarity
                                                                                                     683 AA;
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23-AUG-1999;
03-SEP-1999;
03-SEP-1999;
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Matches 141;
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                                                                                                        Sequence
                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                            286
                                                                                                     180
                                                                                                                                                                                             AGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 466
                                                                                                                                                                                LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVK 406
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                                                                           KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA
                                                                                         ydfggpvggllfglvyspivitglhqsfppielelfnqggsfifatasmaniaqgaacla
                         VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                     Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S, Hayashi M,
Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                             683 AA.
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Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C glutamicum protein fragment
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                                                                                                                                                                                                                                                                                                                                                                            AAG93207 standard; Protein;
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2000JP-0280988.
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Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coryneform bacterium;
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N-PSDB; AAH68426.
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07-APR-2000;
03-AUG-2000;
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tp 362
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Tateishi N,
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from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                     47;
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                                                                                                                                                                                                                                                                                                                Length 683;
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                                                                                                                                                                                                                                                                                                           Score 468.5; DB 22; Length
Pred. No. 6.3e-38;
); Mismatches 206; Indels
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                                                                 Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphorransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation
                                                                                                                                                                   phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the chemicals, for modulating fine chemical production of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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218 tvfglpmvlndysgqvfppliaaiglywvekglkkiipeavqmvfvpffsllimipataf 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 683;
                       Haberhauer
                                                                                                                                                         present invention relates to Corynebacteium glutamicum
                                                                                                                                                                                                                                                                                                       19.8%; Score 468.5; DB 22; 29.8%; Pred. No. 6.3e-38; ive 79; Mismatches 206;
                       Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli protein sequence SEQ ID NO:330.
                        Ħ
                     Schroeder
                                                                                                                                 Claim 32; Page 136; 144pp; English.
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                                                                                                                                                                                                                                                                                                        Query Match 19.8%
Best Local Similarity 29.8%
Matches 141; Conservative
                        B,
                        Kroeger
                                              WPI; 2001-080989/09
                                                                                                                                                                                                                                                                    683 AA;
(BADI ) BASF AG
                     Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2001
                                                                                                                                                                                                                                                                    Sequence
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gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to the sequences required for proliferation acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism (I) have antibacterial and antibiotic activities, and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491 represent oligonuclectides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 --GSFIFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IAIGPAMRWVGDVLAHGLQGLYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 F---GGPVGGLLFGLVYSPIVITGLHQSFPPI----------ELELFNQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 wivsagalgsgifgfinrlliptglhqvlntiawfqigeftnaagtvfhgdinrfyagdg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tagmfmsgffpimmfglpgaalamyfaapkerrpmvggmllsvavtafltgvtepleflf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GVNLRLRWPFFIGIGTAAIGGAL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVL-----TLLLTGFLTF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457376/49
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Best Local Similarity
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                                                                                                                        Escherichia coli.
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                                                                                                                                                                                                WO200148209-A2;
                                                                                                                                                                                                                                                                                                                                       19-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                                                                                                                                       05-JUL-2001
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Length 135;

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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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345 viffaiyfvvfslvirmfnlktpgredkedeivteeansnteegltqlatnyiaavggtd 404
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                                                                                                                                                                                                                             SDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIG 384
                                                                                                                                                                                      571
                                                                                                                                                                                                               385 FDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY 444
                                                                                                       265 AIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSV
                                                                                                                        -----GFLGVVSIDAPDMVMFLVCAVVTFFIAFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoenolpyruvate; sugar phosphotransferase system; PTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                             C.glutamicum phosphoenolpyruvate protein #7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schroeder H,
                                                                                                                                                                                                                                                                                                                                                              AAB66723 standard; protein; 135 AA
 99US-0142691.
99US-0150310.
99DE-1042095.
99DE-1042097.
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                                                                                                                                                                                                                                                                                         632 aqghivagqtplyeikk 648
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                                                                                                                                                                                                                                                                   445 GLGEIEAGANLLNVAKK 461
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-080989/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transformation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200102583-A2.
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                        AAB66723;
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135 AA;

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                                                                                                                386 DTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYG 445
                                                                                                                                Gaps
                                                         326 DAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGF 385
                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Borrelia burgdorferi nucleic acids – used to develo products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                     Antigenic protein; vaccine; Lyme disease; infection; detection.
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9.9%; Score 233.5; DB 20;
Best Local Similarity 34.8%; Pred. No. 2.6e-15;
Matches 46; Conservative 30; Mismatches 51; I
9.9%; Score 234; DB 22;
37.5%; Pred. No. 1.7e-15;
tive 25; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                          B. burgdorferi antigenic protein, f346.aa.
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                                                                                                                                                                                                                                                                      AAY20012 standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH, Erwin AL, Hanson MS,
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                 118 adganssttvikvngk 133
                                                                                                                                                                        446 LGEIEAGANLLNVAKK 461
                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi.
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                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           W09859071-A1
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20-JUN-1997;
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22-JUL-1997
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  Query Match
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Matches
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                                                                                                                                                                                                                                                176 salresnekttlkqvfkvlgqndqilwlafaywfyglgintlnalqlyyfsyilgdargy 235
                                                                                                                                                                                                                                                                                         236 sllytintfvglisasffpslakkfnrnrlfyaciavmllgigvfsvasgslalslvgae 295
                                                                                                                                                                                                                                                                                                                                                                         ---LYLVRR 275
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fiitnlitairigevlldplignaidrtesrwgkfkpwvvgggiisslallalftdfggi 62

    used to develop

                                        ----PVGGL-LFGLVYSPIVI -----TGLHQSFPPIELE-----LFNQGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FIFATASMAN---IAQGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. burgdorferi antigenic protein, t346.aa.
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                                                                                                                                                                                                                                                                                                                                                                         256 VTFF---IAF-----GAAIAYG-----
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97US-0050359.
97US-0053344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrella burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choi GH, Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-189980/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1998;
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22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY53620-21 are encoded by the lactose operon of Lactobacillus bulgaricus, and represent a permease (AAY53620) and beta-galactosidase (AAY53621). The specification describes a mutant L. bulgaricus strain lacking beta-galactosidase activity, because it has a termination (nonsense) mutation in at least one of the coding sequences of the lactose operon. The resulting mutant strain is unable to ferment lactose. Since the mutant strain cannot ferment lactose, fermented milk products produced using it do not have to be cooled to prevent post-acidification. The mutant L. bulgaricus strain of the invention is used for producing a fermented milk product, especially yoghurt. Especially, milk is fermented with a culture of the mutant strain and optionally streptococcus thermophilus in the presence of at least one sugar assimilable by the mutant strain, preferably glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mutant Lactobacillus bulgaricus strain lacking beta-galactosidase activity useful for making fermented milk products, especially yoghurt
319 IALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVD 378
                                                                             379 ILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKT 438
                                                                                                         | :| | :|:|||| | : ::| || ||:: :| |: :| ||:|::| :: |
57 ifvhfgintlnlngkgftrvaeeginvkggeviirldleylkehsesvitpvviansdev 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLITPVLTLLLTG-FLTFIAIGPAM-----RW-----VGDVLAHGLQGLY-DFGG- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                     Amino acid sequence of a permease encoded by the lactose operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 232.5; DB 21; Length 583;
22.2%; Pred. No. 2.1e-14;
tive 74; Mismatches 154; Indels 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactose operon; permease; beta-galactosidase; mutant; yoghurt; beta-galactosidase activity; lactose fermentation; fermented milk product; Streptococcus thermophilus.
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                                                                                                                                                                                                                                                                                                             AAY53620 standard; Protein; 583 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gendre F;
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Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactobacillus bulgaricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brignon P,
                                                                                                                                                               439 GPVNTYGLGEIE 450
                                                                                                                                                                                        : | :|
117 ssie-ysfgrle 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-026146/03.
N-PSDB; AAZ36227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR2778921-A1
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                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                   AAY53620;
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related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.

413 AA;

Sequence

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3;

Length 413;

22;

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SSXS
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                                                                       This sequence represents a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in mannans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                   353 GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 412
                                                                                                                                                                                                                                                                                                                    products for the diagnosis, prevention and treatment of diseases caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ġ
                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                          Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoenolpyruvate; sugar phosphotransferase system; PTS.
                                                                                                                                                                                                                                       7.0%; Score 166.5; DB 20; Length 34.7%; Pred. No. 9.7e-09; Live 21; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schroeder H, Zelder O,
                                                                                                                                                                                                                                                                                                                                                             413 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIE 450
                                                                                                                                                                                                                                                                                                                                                                                          rldleylkehsesvitpvviansdevssie-ysfgrle 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphoenolpyruvate protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 34; Page 139-140; 144pp; English.
                                           Page 161; 275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66722 standard; protein; 413
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99DE-1042095.
99DE-1042097.
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                                                                                                                                                                                                                                                                       34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-080989/09
                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yping or identify; or transformation
                                                                                                                                                                                             135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.glutamicum
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03-SEP-1999;
                                           Claim 12;
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                      Matches
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Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome.
                                                                                                            87 AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
                                                                                                                               that,
                                                                                 218 tvfglpmvlndysgqvfppliaaiglywvekglkkiipeavqmvfvpffsllimipataf 277
                                                                                                                                                                   146 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL 201
                                                                                                                                                                                 Gaps
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                                                      SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a Staphylococcus aureus protein, based on homology with a human or Staphylococcus aureus protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - to isolate antimicrobial compounds, and in vaccines against S.
                              5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 1..126
/note= "residues designated X are not defined the specification"
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of Staphylococcus aureus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DJC,
JM;
                            93;
 7.0%; Score 166.5; DB 2
28.9%; Pred. No. 5.1e-08;
iive 35; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knowles I
Ward JN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Pages 432-433; 989pp; English.
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Rosenberg M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      AAW28051 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0011888
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Query Match
Best Local Similarity 28.99
Matches 54; Conservative
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RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
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Reichard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-424969/39 N-PSDB; AAT84002.
                                                                                                                                                                                                                        202 RLRWPFF 208
                                                                                                                                                                                                                                                   398 rfkktyf 404
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Pratt JM,
                                                                                                                                                                                                                                                                                                                                                  AAW28051;
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believed to be a nerve growth factor or ptsG protein. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in EScherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81501 to AAV81679 represent specifically claimed protein sequences lated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent cifically claimed nucleotide sequences isolated from S. pneumoniae. sequences have antibacterial and antiinflammatory properties.
                                                                                                                                                                                                                                                                                                                                         334 LGSGVAI-VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                     58 kgfkyfvngndhveaggtxlqfdqgyiqqxgynadxivvis-----nsadlgkvelt 109
                                                                                                                                                                                                                                                                                                                                                                                                               393 THFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAG 452
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                             44; Indels 13;
                                                                                                                                                                                                                                                                      DB 18; Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae type 4 protein sequence #56.
                                                                                                                                                                                                                                                                 6.8%; Score 161.5; DB 1
32.8%; Pred. No. 2.8e-08;
ive 25; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY81556 standard; Protein; 449 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB02451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                   Query Match 6.8
Best Local Similarity 32.8
Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-195300/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 mn 111
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                                                                                                                                                                                                                   Sequence
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The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAIFGV----NLRLRWPFFIG-IGTAAIGGALIALFNIKAV-----ALGAAGFLGVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 mmktvtslkeg----aviadg----wam-gnvvarfgttgiftaiimaivtvliyrmcvk 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RWVGDVLAHGL-QGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 LFNQGGSFIFA--TASMANIAQGAA-----CLAVFFLAKSEKLKGLAGASGVSAVLGITE 193
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQG-----TVLPVLVV---- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --aagghfavagefsnmfviaggsgatlglclyiafaskseglkaigrasvvpalfnine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 hnwwikmpeavpegvsrg-----ftalvpgfvvafvvifingllvamgtdifkvia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 ipfgfvsnltnswiglmiiylltgllwivgihganivfafv-splalanmaen-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 -SWILATIEKFLHKRLKGTADFLITPVLTLLTGFLT------FIAIGPAM----
                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                               Length 449;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORFX ORF555 polypeptide sequence SEQ ID NO:1110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | ::: |||| | : || || || || || 412 dlra--vlvalvcafaaflvylpfirvydqklvkeeqgiz 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID 280
                                                                                                                                                                                                                                                                                                                      Mismatches 117;
                                                                                                                                                                                                                                                                           Score 156; DB 21;
Pred. No. 6.5e-07;
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                                                                                                                                                                                                                                                                                                                      48;
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                                                                                                                                                                                                                                                                             6.6%;
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                  449 AA;
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                                                                                                                                                                                                                                                                                                                      85;
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                                                                                                                                                                                                                    Sequence
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antipsoriatic, antiparkinsonian; noctropic; neuroprotective; costeopathic; antiparkinsonian; noctropic; neuroprotective; osteopathic; antiparkinsonian; noctropic; neuroprotective; costeopathic; anticonvulsant; attractivit; cosquiant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensiane. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storrage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemodlobinuria, antiinfammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.5%; Score 154; DB 21;
32.7%; Pred. No. 1.2e-07;
tive 19; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 1038; 5507pp; English.
31-MAR-2000; 2000WO-US08621.
                                            31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                               Shimkets RA, Leach M;
                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 32; Conservat
                                                                                                                                                                                                                                                                            WPI; 2000-602362/57.
N-PSDB; AAC75000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA;
                                                                       02-APR-1999;
05-APR-1999;
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Search completed: March 21, 2002, 16:22:45 Job time: 221 sec

1;

Gaps

4;

43; Indels

32; Conservative

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300 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF 359

360 PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 397 :|| :| :| :| nahhaltittp----egievlvhigldtvmlrgdsypp 107

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                - protein search, using sw model
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protein ĕ

Run on:

US-09-604-231-2 Title:

2363 Perfect score:

1 MAMVFPSLVNGYDVAATMAA......IEAGANLLNVAKKEAVPATP 468 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

hits satisfying chosen parameters: oţ Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
No.	Score	Match	Match Length	BB	QI	Description
٦	1058.5	44.8	651	-	PTSA_PEDPE	P43470 pediococcus
7	953.5	40.4	664	Н	PTSA_STRMU	
m	701	29.7	480	Н	PTSB_STAXY	P51184 staphylococ
7	678	28.7	474	П	PTSB_PASMU	
2	657	7	609	-	PTBA_BACSU	
9	646	27.3	479	Н	PTSB_VIBAL	P22825 vibrio algi
7	640	27.1	631	Н	PTBA_ERWCH	
80	570	4	470	Н	PTTB_BACSU	P39794 bacillus su
σ	567.5	4	625	Н	PTBA_ECOLI	P08722 escherichia
10	492	0	456	Н	PTSB_SALTY	P08470 salmonella
11	489	٥.	456	-1	PTSB_KLEPN .	P27219 klebsiella
12	462.5	φ.	674	~	PTGA_CORGL	Q45298 corynebacte
13	406	ζ.	459	Н	SACX_BACSU	
14	390	9	460	-	PTSB_BACSU	P05306 bacillus su
15	367	15.5	473	-1	PTTB_ECOLI	P36672 escherichia
16	321.5	m.	669	Н	PTGA_BACSU	P20166 bacillus su
17	317.5		651		PTAA_KLEPN	
18	298.2	•	648	H	PTAA_ECOLI	
19	294.5		324	-	PTGA_BACST	
20	287.5	12.2	631		YBFS_BACSU	
21	270.5	Ξ.	485	7	PTDA_ECOLI	
22	256	ö	189	~	PTGA_BORBU	
23	255		. 168	٦	YPQE_BACSU	P50829 bacillus su
24	254.5	Ö	634	٦	LACY_STRTR	P23936 streptococc
25	250.5	ö	474	Н	YFEV_ECOLI	
26	249.5		154	-4	PTGA_MYCCA	P45618 mycoplasma
27	246	10.4	168	<del></del> i	PTGA_ECOLI	
28	244.5	10.3	482	Н	PTSB_VIBCH	Q9kvd9 vibrio chol
29	24	10.3	168	Н	PTGA_SALTY	P02908 salmonella
30	238.5	٠	165	Н	PTGA_HAEIN	P45338 haemophilus
31	233	6.6	627	Н	LACY_LACDE	P22733 lactobacill
32	231.5		161	٦	PTGA_BUCAI	Q9wxi7 buchnera ap
33			940	-	PTGA_MYCPN	9 mycoplasr

P43466 pediococcus		Q48624 leuconostoc	P32154 escherichia	P54745 escherichia	P54715 bacillus su	P32672 escherichia	P23387 rhodobacter	P23355 xanthomonas			P24400 lactobacill
RAFP_PEDPE	PTGA_MYCGE	LACY_LEULA	PTVB_ECOLI	HRSA_ECOLI	PTIB_BACSU	PTWC_ECOLI	PTFB_RHOCA	PTFB_XANCP	PTMA_BUCAI	PTFA_MYCPN	PTLB_LACCA
-	~	7	_	_	٦	Н	Н	Н	_	٦	Н
641	806	689	483	658	527	359	578	580	632	694	577
9.4	9.8	7.0	6.7	6.4	6.1	5.8	5,5	5.4	5.2	5.2	5.1
221	204	165.5	159	151.5	144.5	136.5	130	126.5	123.5	122	120.5

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PPEL.0;
Leenhouts K.K.J., Bolhuis A.A., Kok J.J., Venema G.G.;
Submitted (XXX-1994) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRNVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); ITA TRANSFERS ITS
PHOSPHORYLATION SITE (THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIABC COMPONENT (EIIABC-SCR) (SUCROSE-PERMEASE IIABC COMPONENT) (FUCSPHOTANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pediococcus pentosaceus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- CATALTICE ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
-:- SUBCELLULAR LOCATION: INTEGRAL MEBRRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRR01127; PTS_EIIA.
InterPro; IRR011926; PTS_EIIA.
InterPro; IRR0119352; PTS_EIIA.
InterPro; IRR011936; PTS_EIIA.
InterPro; IRR03356; PTS_EIIA.
InterPro; IRR03356; PTS_EIIA.
InterPro; IRR03376; PTS_EIIA.
InterPro; PRO31TE; PRO31TE; PTS_EIIA.
InterPro; PTS_EIIA.
InterPro; IRR03376; PTS_EIIA.
InterPro; PTS_EIIA.
InterPro; IRR03376; PTS_EIIA.
InterPro; PTS_
                                                                                                           651 AA
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z32771; CAA83668.1; -. EMBL; L32093; AAA25567.1; -. HSSP; P20166; 1AX3.
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pediococcus
                                                                                                     PTSA_PEDPE
P43470;
RESULT 1
PTSA_PEDPE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           540
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                      MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-UUL-1999 (Rel. 13, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC ILABC COMPONENT (EILABC-SCR) (SUCROSE-PERMEASE ILABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGLAGASCVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.; "Characterization and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans
                    EIIB DOMAIN.
EIIC DOMAIN.
EIIA DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
W; C87BAO9D550A77F8 CRC64;
                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                     Mismatches 151; Indels
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                                                                                                                                                                                                                                                                              Score 1058.5; DB Pred. No. 1.2e-62;
                                                                                                                                                                                                                                                    44.8%; Su-
46.7%; Pred
78; }
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Transmembrane
                                                                                                                                                                                           68454 MW;
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324
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                                                                                                                                                                                        651 AA;
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Phosphorylation;
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324
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Matches
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                  194 MIMVAPGAANIIGLAANAPISKAATIGAYTGFWNIFGLHVTQASYTYQVIPVLVAVWLLS 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAMVFPSLVNGYDVAATMAAGEMP-----MWSLFGLDVAQAGYQGTVLPVLVVSWILA 53
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HOSPHORYLATION (BY SIMILARITY).
HOSPHORYLATION (BY SIMILARITY).
809E63E32281A9A1 CRC64;
                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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EIIC DOMAIN.
EIIA DOMAIN.
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Pfam; PF00367; PTS_EIIB; 1.
Pfam; PP02378; PTS_EIIE; 1.
ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS00371; PTS_EIIA; 1.
PROSITE; PS01035; PTS_EIIA_1; 1.
MEDLINE=93329360; PubMed=8336109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
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InterPro, IPR001127, PTS_EIIA.
InterPro, IPR001996, PTS_EIIB.
InterPro, IPR003352, PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation; Transmembrane
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Best Local Similarity
Matches 205; Conserv
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MOD_RES
SEQUENCE
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Transferase;

system;

Phosphotransferase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagner E., Goetz F., Bruecker R.;
"Cloning and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system from Stabhylococcus xylosus.";
Mol. Gen. Genet. 241:33-41(1993).

-I-FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT FUNCTION: THE IIS A COMPONENT OF THE PROSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERAES SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRABE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                     340
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
15-UL-1998 (Rel. 36, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-BERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
                     547
                                                                                                                                      400
                                                                                                                                                                        603
                                                                                                                                                                                                      401 QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY-GLGEIEAGANLLNVA 459
                                                                                                                                                                                                                                          663
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                   VPAGTTKAEAEAPAEFSNDST-----IIQAPLTGEAIALSSVSDAMFASGKLGSGVAI
                                                                                                   VEEAIEEVQ-EIPEEAASAANKAQVTDEVLAAPLAGEAVELTSVNDPVFSSEAMGKGIAI
                                                                                                                                   341 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK
                                                                                                                                                        604 ADQKIKKGDVLGTFDSDKIAEAGLDNTTMFIVTNTADYASVETLASSGTVAVGDSLLEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                                                                                                                               480 AA.
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIB; 1.
ProDom; PD001476; PTS_EIIB.1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-DSM 20267 / C2A;
MEDLINE-94049686; Pubmed-8232209;
                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 34, Created)
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InterPro; IPR003352; PTS_EIIC.
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                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus xylosus.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

Fro. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

FURTION: THIS IS A COMPONENT OF THE PHOSPHOENCEPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHOHEN); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
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BC COMPONENT)
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6
                                  EIIB DOMAIN.
EIIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
AB4EID9785D84E47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                      Length 480;
                                                                                                                                                                                                          81; Indels
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR)
PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, 8 (EC 2.7.1.69) (EII-SCR).
SCRA OR PTSB OR PM1846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE SUGAR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + :
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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                                                                                                                                                                      DB 1;
Sugar transport; Tra
ne; Phosphorylation.
                                                                                                                                                                    ; Score 701; DB 1;
; Pred. No. 3e-39;
49; Mismatches
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-!- SIMILARITY; CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY; CONTAINS A PTS EIIC DOMAIN.
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                      Inner membrane;
                                                                                                              51326 MW;
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Best Local Similarity 51.4%;
Matches 146; Conservative 4
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Q9CJZ2;
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DOMAIN
MOD_RES
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P40739; Q45661;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-BGL)
(BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
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D26FA1A059603C01 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
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474 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    MOI. Gen. Genet. 250:761-766(1996).

-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
MEDLINE-95189730; PubMed-7883710; le Coq D.G., Lindner C., Krueger S., Steinmetz M., Stuelke J.; le Coq D.G., Lindner C., Krueger S., Steinmetz M., Stuelke J.; "New beta-glucoside (bgl) genes in Bacillus subtilis: the bglp gene product has both transport and regulatory functions similar to those Of BglF, its Escherichia coli homolog."; Je Bacteriol. 177:1527-1535(1995).
                                                                                                                                                                                  Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.; "Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci."; Microbiology 141:337-343(1995).
                                                                                                                                                                                                                                                                                                              MEDLINE-96204517; PubMed-8628237;
Beloin C., Hirschbein L., le Hegarat F.;
"Suppression of the Bgl+ phenotype of a delta hns strain of
Escherichia coli by a Bacillus subtilis antiterminator binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ase system; Sugar transport; Transfer
Transmembrane; Complete proteome.
BIB DOMAIN.
BIIC DOMAIN.
COPE BIIR DOMAIN.
DEST PHOSPHORYLATION (BY SIME STATE STA
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Pfam; PF00367; PTC_EIIB, 1.
Pfam; PF003767; PTS_EIIB, 1.
ProDom; PD001476; PTS_EIIB; 1.
ProDom; PD002243; PTS_EIIB; 1.
PROSITE; PS000371; PTS_EIIA; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Phosphotransferase system; Sugar tran
                                                                                                                                           STRAIN=168 / BGSC1A1;
MEDLINE=95219088; PubMed=7704263;
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EMBL; D31856; BAA06552.1; --
EMBL; D29985; BAA06256.1; --
EMBL; X85408; CAA59697.1; --
EMBL; Z89124; CAB15963.1; --
PIR; S47174; --
HSSP; P20166; 1AX3.
Subtilist; BG10934; bg1P.
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
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DOMAIN 1
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Gene 95:17-23(1990)
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Nucleotide
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BC COMPONENT)
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                                                                                                                                                     Length 609;
                                                                                                                                                                     84; Mismatches 181; Indels
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01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR)
PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II,
(EC 2.7.1.69) (EII-SCR).
                                                                                                                            CRC64;
                                                                 A -> S (IN REF. 3).
L -> F (IN REF. 2).
E -> G (IN REF. 2).
A -> S (IN REF. 2).
DG -> HR (IN REF. 2).
I -> M (IN REF. 2).
G -> S (IN REF. 2).
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                                                                                                                                                    27.8%; Score 657; DB 1; 33.4%; Pred. No. 3.1e-36;
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MEDLINE=91071601; Pubmed=2174811;
Blatch G.L., Scholle R.R., Woods D.R.
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609 AA;
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Best Local Similarity
Matches 153; Conserv
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NCBI_TaxID=663;
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                                                                                                                                                                                                                              repressor-encoding gene (scrR).";
Gene 101:45-50(11991).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
THE SUGAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
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sequence and analysis of the Vibrio alginolyticus sucrose
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-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-1- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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PHOSPHORYLATION (BY SIMILARITY).
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FBF906B5170E3EB7 CRC64;
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46.5%; Pred. No. 1.3e-35;
Live 54; Mismatches 87; Indels
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
Phosphotransferase system; Sugar transport; Tra
Transmembrane; Inner membrane; Phosphorylation.
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SEQUENCE OF 1-12 FROM N.A.
MEDLINE-91285433; PubMed=2060795;
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InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; I
Pfam; PF02378; PTS_EIIC; I.
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PIR; JQ0781; JQ0781.
HSSP; P05053; 11BA.
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Matches 128; Conservative
                                 uptake-encoding region.";
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                                                                                                                                                                                                                                                                                                                                                                                                     Hassouni M., Henrissat B., Chippeux M., Barras F.;

el Hassouni M., Henrissat B., Chippeux M., Barras F.;

"Nucleotide sequences of the arb genes, which control beta-glucoside utilization in Erwinia chrysanthemi: comparison with the Escherichia coli bgl operon and evidence for a new beta-glycohdrolase family including enzymes from eubacteria, archeabacteria, and humans.";

J. Bacteriol. 174:765-777(1992).

-I. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERSE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS HE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS PHOSPHORYLATION SITE (THE DONOR IN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ÁCTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
                                                                                                               01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, BETA-GLUGOSIDES-SPECIFIC ITABC COMPONENT (EITABC-BGL)
(BETA-GLUCOSIDES-PERMEASE ITABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON ARBG (BY SIMILARITY).
                                                                                                                                                                                                                                                               Erwinia chrysanthemi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
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SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00358; PTS_EIIL.
Pfam; PF00376; PTS_EIILB.1.
Pfam; PF003778; PTS_EIILB.1.
ProDom; PD00243; PTS_EIIB; 1.
ProSom; PD00243; PTS_EIIB; 1.
PROSITE; PS010371; PTS_EIIB.1.
PROSITE; PS01035; PTS_EIIB.1.
PROSITE; PS01035; PTS_EIIB.1.
PROSITE; PS01035; PTS_EIIB.1.
PROSITE; PS01035; PTS_EIIB.2.
PROSITE: PS01035; PTS_EIIB.2.
PROSITE: PS01035; PTS_EIIB.2.
PROSITE: PS01035; PTS_EIIB.2.
PROSIDE: PS01037; PTS_EIIB.2.
PS01
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PHOSPHORYLATION (
PHOSPHORYLATION (
PHOSPHORYLATION (
                                                                             631 AA
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                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92121114; PubMed-1732212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P20166; 1AX3.
InterPro; IPR00127; PTS_EIIA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M81772; AAA24814.1; -.
                                                                             STANDARD;
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309
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                                                                                                                                                                                                                                                                                                          Pectobacterium.
                                                                           PTBA_ERWCH
P26207;
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PTBA_ERWCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAFSAAIFGITEPAVYGVTLPLRRPFIFGCIGGALGAAVWGYAHTTMYSFGFPSIFSFTO 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 VIPPTGVDSSVWAAVIGTLLAFAFAALTSWSFGVPKD----ETQPAAADSPA--VLAETQA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAI 419
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 LVHPSMIAAFN---AMQAPDHSTLHFLGIPITFINYSSSVIPILFASWVSCKLEKPLNRW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LKGTADFLITPVLTLLIGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 QVCVIFGLHWGFVPLMLNNFSVIGHDTLLPLLVPAVLGQAGATLGVLRTQDLKRKGIAG 360
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STRAIN-168 / MARBURG;
MEDLINE-97074649; Pubmed-8917076;
Schoeck F., Dahl M.K.;
"Analysis of DNA flanking the treA gene of Bacillus subtilis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                               3 MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTTB_BACSU STANDARD; PRT; 470 AA.

197974; 034771;
01-FEB-1995 (Rel. 31, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
(TREIALOSE-PERMEASE IIBC COMPONENT (EIIBC-TRE)
COMPONENT) (EC 2.7.1.69) (EII-TRE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDAPDMVMFLV-CAVVTFFIAFG-AAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVS
                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                   Length 631;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                           DOBD27A36BFFFDF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                 27.1%; Score 640; DB 1; 33.8%; Pred. No. 4.2e-35;
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                                                                                                                                                                                                                                                           631 AA;
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Bacillus subtilis.
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the European Bioinformatics Institute. There are no restrictions on its
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R Subtlinst; BG11009; trep.

DR InterPro; IPR001996; PTS_EIIB.

DR InterPro; IPR001996; PTS_EIIB.

DR Ffam; PF00377; PTS_EIIC; 1.

DR Pfam; PF00376; PTS_EIIC; 1.

DR ProDom; DF00176; PTS_EIIB; 1.

DR PROSTE; PS01035; PTS_EIIB; 1.

DR PROSTE; PS01035; PTS_EIIB 11.

Transmembrane; Inner membrane; Phosphorylation; Complete proteome.

**Transmembrane; Inner membrane; Phosphorylation; Phosphory
                                                                                                                                                                                                                                                                                                  Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; "Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 40 6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes for trehalose metabolism and acetoin utilization.";
Microbiology 142:3057-3065(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR - PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EILC DOMAIN.
genes encoding a putative specific enzyme IITre and a potential regulator of the trehalose operon.";
Gene 175:59-63(1996).
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                general stress response protein.";
Gene 194:191-199(1997).
                                                                                                                                                                                                                                                                  STRAIN-AC327;
MEDLINE-97417488; PubMed-9272861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95379486; PubMed=7651129;
                                                                                          STRAIN=AC327;
MEDLINE=97124190; PubMed=8969503;
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EMBL, D83967; BAA23409.1; -.
EMBL, D86417; BAA22289.1; -.
EMBL; X80203; CAA56494.1; -.
EMBL, 299108; CAB12609.1; -.
HSSP; P05053; 11BA.
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130
180
203
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                                                                            SEQUENCE FROM N.A.
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GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPIVITGLHQSFPPIELELFNQ - - GGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                                                                                                                                                                                                                                                                                                                                 63 LKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVY 122
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08722;
1.AGG-1988 (Rel. 08, Last sequence update)
20.AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC ITABC COMPONENT (EIIABC-BGL)
PTS SYSTEM, PETA-GLUCOSIDES-PROITE (INABC COMPONENT) (PHOSPHOTRANSFERASE
(BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schnetz K., Toloczyki C., Rak B.;
Betra-flucoside (bgl) operon of Escherichia coli K-12: nucleotide
sequence, genetic organization, and possible evolutionary
relationship to regulatory components of two Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bramley H.F., Kornberg H.L.;
"Nucleotide sequence of bglC, the gene specifying enzymeIIbgl of PEPs:ugar phosphotransferase system in Escherichia coli Kl2, and overexpression of the gene product.";
J. Gen. Microbiol. 133:563-573(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                          Score 570; DB 1; Length 470;
Pred. No. 1.2e-30;
                                                                                                                                                                                                                                                                                     99; Indels
                                                                                                                             -> S (IN REF. 1).
-> L (IN REF. 1 AND 4).
-> G (IN REF. 1 AND 4).
7A741850A2697D53 CRC64;
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                                                                                                                                                                                                                                                                                   54; Mismatches
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                                 POTENTIAL.
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[3]
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42.8%;
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470 AA;
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Matches 116;
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                                                                                                                                                                                        AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                     SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
                                                                                                                 Genomics 16:551-561(1993).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | EMBL; L10228; AAAC76745.1; - |
| R EMBL; L10228; AAAC76745.1; - |
| R PIR; C25977; C25977; C25977. |
| R PIR; A47616; A47616; A47616. |
| R PSP; P20166; 1AX3. |
| R BCOGGARE; BC10115; bG1R. |
| R InterPro; IPR001127; PTS_EIIA. |
| InterPro; IPR00135; PTS_EIIA. |
| R InterPro; IPR00358; PTS_EIIB. |
| R Pfam; PF00378; PTS_EIIB. |
| R Pfam; PF00378; PTS_EIIB. |
| R Pf00m; PD00176; PTS_EIIB. |
| R Probom; PD00176; PTS_EIIA; 1. |
| R PROSTITE; PS010176; PTS_EIIA; 1. |
| R PROSTITE; PS01035; PTS_EIIA; 1. |
| R PROSTITE; PS01036; PTS_EIIA; 1. |
| R PROSTITE; PS01
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CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL BEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=93315143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coli
                                                                                               genome: organizational symmetry around the origin of replication.";
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Ebner R., Lengeler J.W.; "DNA sequence of the gene scrA encoding the sucrose transport protein "DNA sequence of the gene scrA encoding the sucrose transport protein EnzymeII(Scr) of the phosphotransferase system from enteric bacteria: homology of the EnzymeII(Scr) and EnzymeII(Bgl) proteins."; Mol. Microbiol. 2:9-17(1988).
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01-UN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
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                                                                                                                                      Gaps
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; Score 567.5; DB 1;
; Pred. No. 2.5e-30;
91; Mismatches 211;
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MEDLINE-88216186; PubMed=3285123;
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                                                                                                                                      Conservative
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1. Bacteriol. 173:449-456(1991).

2. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTORNAREBRASE SYSTEM (PTS). A MAJOR CARBOHYBARE ACTIVE TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO THE SUGAR. EIIBC-SCR BELONGS TO THE EIIBC DOMAIN TYPE AND LACKS A COVALENTLY BOUND EIIA DOMAIN. INSTEAD, EII-SCR-MEDIATED PHOSPHORYLATION OF SUGGROSE REQUIRES THA ACTIVITY OF ENZYME IIA-CLA COMPONENT OF THE MAJOR GLUGOSE TRANSPORT SYSTEM.

2. CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR - SUGAR PROSPHARE.

2. CHALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR - SUGAR PROSPHARE.

3. SUBJEACH STANSMENDEN A PROFILE DOMAIN. INNER MEMBRANE.

3. SIMILARITY: CONTAINS A PTS EIIG DOMAIN.
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Transmembrane; Inner membrane; Phosphorylation.
Hardesty C., Ferran C., Direnzo J.M.; "Plasmid-mediated sucrose metabolism in Escherichia coli: "Plasmid-mediated sucrys the structural gene for a phosphoenolpyruvate-dependent sucrose phosphotransferase system
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EIIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
98A6F1620AE50885 CRC64;
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38.5%; Pred. No. 1.7e-25;
ive 52; Mismatches 100;
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InterPro: IPR003352; PTS_EIIC.
Pfam: PF00376; PTS_EIIE; 1.
ProDom: PD001476; PTS_EIIB; 1.
PR0SITE: PS01035; PTS_EIIB_CYS; 1.
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EMBL, Y00541; CAA68605.1; ALT_SEQ.
EMBL, M38416; AAA98418.1; --
HR; S01036; WQEBST.
HSSP, P05053; 11BA.
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STRAIN-103-5PI4 / KAY2026;

XM MEDLINE-9131213; PubMed-1649946;

MEDLINE-9131213; PubMed-1649946;

Schmid K., Ebner R., Jahreis K., Lengeler J.W., Titgemeyer F.;

A sugar-specific point, ScrY, is involved in sucrose uptake in enteric bacteria.";

Mol. Microbiol. 5:941-950(1991).

C. !- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN COMPAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN COMPAIN TYPE AND LACKS A PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO THE SUGAR. BIIBG-SCR BELONGS TO THE EIIBC DOMAIN TYPE AND LACKS A COVALENTLY BOUND EIIA DOMAIN. INSTEAD, EIL-SCR MEDIAPED PHOSPHORYLATION OF THE MAJOR GLUCOSE TRANSFORT SYSTEM.

C. COVALENTLY BOUND EILA DOMAIN. INSTEAD, EIL-SCR WEDIAPED PHOSPHONELY OF THE MAJOR GLUCOSE TRANSFORT SYSTEM.

C. -I- CATALYITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
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                                                                         PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EC. 2.7.1.69) (EII-SCR).
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                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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PROSTER; PS01035; PTS_EIIL_CYS; 1.
Phosphotransferase system; Sugar transport; Transferase; Transmembrane; Inner membrane; Phosphorylation.
                                                01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIEC COMPONENT (1
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Interpro; IPR003352; PTS_EIIC.
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Pfam; PF02378; PTS_EIIC;
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HSSP; P05053; 1IBA.
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PTSB_KLEPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and nucleotide sequence of enzyme II of Brevibacterium lactofermentum phosphotransferase system.";
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLEYRUVAE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONAIN WHICH FINALLY TRANSFERS IT FUNDENCE THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
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                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, GLUCOSE-SPECIFIC INAC COMPONENT (EIIABC-GLC) (GLUCOSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum (Brevibacterium flavum).
                                   Score 489; DB 1;
Pred. No. 2.6e-25;
                                                                                                                                                                                                                                                                                                                                                                                           674 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPONENT) (EC 2.7.1.69) (EII-GLC/EIII-GLC)
                                                                                                                                                                                                                                                                                                LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
                                                                                                                                                                                                                                                                                                                          PGMAIVQASSLLNYIIGMAIAFAVAFALSL 447
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                   20.7%;
38.5%;
                                                            Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 13869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pBSBG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUGAR.
                                                                                                                                                                                                                                                                                                                                                                                         PTGA_CORGL
Q45298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoon K.-H.
                                    Query Match
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                                                  Local
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AIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-G 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 EAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 TVFGLPMVLNDYSGOVFPPLIAAIGLYWVEKALKKIIPEAVOMVFVPFFSLLIMIPATAF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 YDFIQGPMGAWNFACFGLVTGVFLIALKEKNRAMRQVSLGGMLAGLLGGISEPSLYGVLL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGAS--GVSAVL--GITEPAIFGVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PDATAAPV------PAGTTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTSMLLVLFFDYRSDAERDEAKAQMAAAEQTNNTPAAPAAPAAPAAGAAAAGGAAGAT-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      512 VATKPRLAAGQLVEITSPLEGHAVPLSEVPDPIFAAGKLGPGIAIEPTGNTVVAPADATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY). SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67A75AAF76E42FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 462.5; DB 1;
; Pred. No. 2.2e-23;
79; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 416 IDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     628 PEFIRSKNLPLITPVVVSNANKFGEIVGIEAAQADATTTVIKV
                                                                                                                                                                                                                                                ase system; Sugar transport; Transmembrane; Plasmid.
7 EIIB DOMAIN.
674 EIIB DOMAIN.
146 POTENTIAL.
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POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                        PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                      InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR003152; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIB; 1.
ProDom; PD001476; PTS_EIIC; 1.
ProDom; PD001476; PTS_EIIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.6%;
                                                                                                                                                                                                                                                     Phosphotransferase system;
EMBL; L18875; AAA22992.1;
HSSP; P08837; 2F3G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        674 AA;
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Matches 139; Conserv
                                                                                                                                                                                                                                                                      Phosphorylation;
                                                                                                                                                                                                                                                                                                                                 542
1126
1162
1193
225
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303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of the sacS locus of Bacillus subtilis reveals the presence of two regulatory genes."; Gene 90:153-155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees."; 401. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionoscu M., Lubochinsky B., Marcelino L., Moszer I., Presecan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIIB DOMAIN.
EIIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glaser P., Kunst F., Debarbouille M., Vertes A., Danchin A., Dedonder R.;
                                                                                                                                                                                                                                                                                       Zukowski M.M., Miller L., Cogswell P., Chen K., Aymerich S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pranscription regulation; Transferase; Phosphorylation;
                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
02-ANG-2001 (Rel. 40, Last annotation update)
NEGATIVE REGULATORY PROTEIN OF SACY.
459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95020537; PubMed-7934828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92216127; PubMed-1806041;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-90337338; Pubmed-2116367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 348-459 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M2933; AAA75335.1; -. EMBL; X52480; CAA36719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X73124; CAA51570.1; -. EMBL; Z99123; CAB15867.1; -. PIR; JU0293; JU0293. PIR; S16421; S16421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00367; PTS_EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02378; PTS_EIIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SubtiList; BG10560; sacX
                                                                                                                        SACX OR SACS OR IPA-14R.
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P05053; 11BA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                       NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                            Steinmetz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168;
SACX_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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FITTER BRANCH BR
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"Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384[1993].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(PC 27.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 IWGLHIPMMGYQGSMIPILLSVFVMSKIEKLLKSIVPKSLDVVIIPFITVMVTGCLALIV 265
                                                                                                                                                                                                                                                                                                                                                                                                              266 MNPAASIIGQIMTQSIVYIXDHAGIAAGALFGGIXSTIVLSGLHHSFYALEATLLANPHV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 WPFFIGIGTA---AIGGALIALFNIKAVALGAAGFLGVVSIDAP------DMVMFLVC 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                28 LFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSFIFATASMANIAOGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLR
                                                                                                                                                                                                                                                                                                                                                                                IGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF---NQ
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MEDLINE-95020537; PubMed=7934828;
Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88097369; PubMed-3122206;
Fouet A., Arnaud M., Klier A., Rapoport G.;
"Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria.";
Proc. Natl. Acad. Sci. U.S.A. 84:8773-8777(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON SACT
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
A5C4E996ECDA3D40 CRC64;
                                                                                                                                             17.2%; Score 406; DB 1; Length 459; 37.9%; Pred. No. 7.7e-20;
                                                                                                                                                                                                       88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Firmicutes, Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 AA
                                                                                                                                                                         ; Pred. No. 7.7e
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                         49024 MW;
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 AV----VTFFIAF 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 AVSAFIATLFLGF 454
   136 1
433 4
459 AA;
                                                                                                                                                                         Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUGAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1988
01-NOV-1988
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTSB_BACSU
                                                            SEQUENCE
                                                                                                                                                   Query Match
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NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blattner F.R.;
                                                                                                                                                                                      B4240
                                                                                                                                                                                                                                                                                                                                                                        STRAIN-K12
                                                                                                                                                                                      FREB OR
     936672
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
SIMILARITY: 57% IDENTITY WITH THE NEGATIVE REGULATORY PROTEIN OF SACY.
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  CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphotransferase system; Sugar transport; Transferase; Transmembrane; Phosphorylation; Complete proteome.

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BIIC DOMAIN

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BIIC DOMAIN.
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                        PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
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EMBL; X73124; CAA51605.1; --
EMBL; Z99123; CAB15831.1; --
PIR; A39938; A39938.
PIR; S39704; S39704.
SubtList; B610595; SaCP.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001996; PTS_EIIC.
Pfam. DF00577; PMS_EIID.
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Pfam; PF02378; PTS_EIIC; 1
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473 AA.

PRT;

STANDARD;

PTTB\_ECOLI ID PTTB\_ECOLI

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"The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE CYVALENTLY BOUND BITA DOMAIN. THE BIB DOMAIN CONTAINS THE TRANSPORT SYSTEM. IT BELONGS TO THE BILD COMPAINS THE PHOSPHORYL TRANSFER DOMAIN. THE IID DOMAIN CONTAINS THE PHOSPHORYL TRANSFER DOMAIN. THE BILL-TRE-MEDIATED PHOSPHORYLATION OF TRANSFERIE CHURCHS TRANSPORT SYSTEM.

- TRANSFORT SYSTEM SYSTEM SYSTEM IS A COMPONENT OF THE MAJOR GLUCOSE TRANSPORT SYSTEM.

- I CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHORY SYSTEM.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.

- SIMILARITY: CONTAINS A PTS BILD DOMAIN.
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       01-JUN-1994 (Rel. 29, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE-PERMEASE LIBC COMPONENT) (PHOSPHOTTRANSFERASE ENZYME II, BC COMPONENT)
(FC 27.1.69) (EII-TRE).
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"Molecular analysis of treB encoding the Escherichia coli enzyme II
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
Phosphotransferase system; Sugar transport; Transferase;
Transmembrane; Inner membrane; Phosphorylation; Complete proteome.
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                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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STRAIN-412 / MG1655;
MEDLINE-9533452; Pubmed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific for trehalose.";
J. Bacteriol, 177:4043-4052(1995).
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MEDLINE-97426617; PubMed-9278503;
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EMBL; AE000495; AAC77197.1; -.
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InterPro; IPR003352; PTS_EIIC.
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                                                 PHOSPHORYLATION (BY SIMILARITY).
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GL -> PF (IN REF. 1).
GL -> PF (IN REF. 1).
GGTPILGIVLG -> AQRRSLVSCLA (IN REF. 2).
MISSING (IN REF. 1).
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PGILSIQPSWOVENLAMALALITPIVLTSFIYORKYRLGT
LDIV -> RNSLDSTELLAGVCAGNGYRHHPDCTHLVYLS
AEIPPGHAGHCLIFFGAQLRSHSQE (IN REF. 1).
7437F88228624944 CRC64;
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Best Local Similarity 30.1%; Pred. No. 2.9e-17;
Matches 80; Conservative 63; Mismatches 109; Indels 14; Gaps
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  EIIB DOMAIN.
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046072 corynebacte
045622 bacillus sp
P94470 bacillus st
092kh9 clostridum
093x3 staphylococ
094k12 vibrio chol
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"Characterization of the divergent sacBK and sacAR operons, involved in sucrose utilization by Lactococcus lactis.";
J. Bacteriol. 181:1924-1926(1999).
Bacteriol. 181:297015; CAB09690.1;
HSSP; P45618; 20PR.
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42.9%; Pred. No. 9.4e-47;
ive 89; Mismatches 145; Indels 36; Gaps
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Lactococcus.
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR00358; PTS_EIIC.
Pfam; PP00358; PTS_EIIA.; 1.
Pfam; PP00378; PTS_EIIB; 1.
Propom; PD002243; PTS_EIIC, 1.
PROSITE; PS00371; PTS_EIIA,; 1.
PROSITE; PS01035; PTS_EIIA.; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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MEDLINE=99173919; Pubmed=10074089;
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Best Local Similarity 42.99
Matches 203; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Nucleic Acids Res. 28.4317-4331(2000).
EMBL, APO01508; BAB04015.1;
InterPro; IPR001195; PTS_EIIA.
InterPro; IPR0011996; PTS_EIIB.
Fig. FFR00358; PTS_EIIC.
Pfam; PF00358; PTS_EIIB: 1.
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT
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Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
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Probom; PP002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA] 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
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"Analysis of a catabolic operon for sucrose transport and metabolism in Clostridium acetbutylicum ATCC 824.";

EMBL; AF205034; AAF35839.1; -
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001359; PTS_EIIA.
InterPro; IPR001359; PTS_EIIA.
InterPro; IPR001354; Trypsin.
Pfam; PF00358; PTS_EIIA.
InterPro; IPR00358; PTS_EIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR 62
                                                                                                                                                                                                                                                    235 GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTK
                                                                                                                                                                                                                                                                             Clostridium acetobutylicum.
Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407 AGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD002243; PTS_EITA; 1.
PROSITE; PS00371; PTS_EIIA_1; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
SEQUENCE 627 AA; 67596 MW; B835AB0238FCA436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.1%; Score 759.5; DB 2;
llarity 36.7%; Pred. No. 2.5e-35;
Conservative 80; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 824;
MEDLINE=20391269; PubMed=10937490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=ATCC 824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1488;
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01-OCT-2000 (
01-JUN-2001 (
SCRA.
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Best Local Si
Matches 163;
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SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE 01;
STRAIN=-20406833; PubMed=10952301;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 DATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLVYPTLV-----VLTEGE-PLYTLFTGTIFESPVHITFLGIPVILMSYATSVIPILL 234
                                                                                                                                                                                                                            295 NLSPIIAGAFLGGFWQVFVIFGLHWGLIPIAINNLVVQGSDPVLAMVFAASFAQIGAVAA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                            DFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLA
                                                                                                                                                                                                                                                                                                            VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI
                                                                                  VSWILATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLY
                                                                                                                                                                                                                                                                                                                                                                                                                         KAVALGAAGFLGVVSI - - - - DAPDMVMF - LVCAVVTFFIAFGAAIAYGLYLVRRNGSIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGYIIGGLGIFGIPSFLHPADGMDAGFWGIVIAVVVAFV.LGFILTYLFGLKSGNASDEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
SUCROSE-SPECIFIC IIBC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479
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Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholerae.";
Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=666;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the alkaliphilic bacterium Bacillus
T "Complete genome sequence comparison with Bacillus subtilis.";
In halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:437/4331(2000).
RMELAPOOLSO9; BAB04314.1...
RMELAPOOLSO9; BAB04314.1...
RICETPO: IPR001127; PTS_EIIA.
RICETPO: IPR001127; PTS_EIIA.
RICETPO: IPR003152; PTS_EIIA.
REPEAM: PF00352; PTS_EIIA.
REPEAM: PF00352; PTS_EIIC.
REPEAM: PF00353; PTS_EIIC.
REPEAM: PF00354; PTS_EIIA; 1...
REPEAM: PF00371; PTS_EIIA.
REPEAM: PF00
                                                                                                                                    122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                                                                                                                                                                                                                                         416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLKGTADFLITPVLTLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGPYGGLLFGLY 121
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                                                                                                                                                                                                                                                                                 GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
                                                                                                                                                                                                                                                                                                                                                              SI---DAPDMYMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                      417 IFYPEDGRGFVAFVIAIIISFVLA----AVLTYIVGFKDPVDDEDTLSNESGSENEVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGOLVSPVSGKIVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, ETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ||||:| ||::::| |: | | |: |::| |
588 RITAAGYDVITPVLITNAKQFSNVQTTDKREVTSEDLLIHVIK 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.5%; Score 673.5; DB 2; 34.0%; Pred. No. 1.8e-30; Live 78; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          636 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AMVFPSLVNGYDVAATMAAGEMPMWSLF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 163; Conserv
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**09KF90** 

RESULT Q9KF90

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Gaps
                                                      Length 479
                                                                                          Indels
50292 MW; DC0E129229957E3C CRC64;
                                                                                          87;
                                                    27.9%; Score 659; DB 2;
49.3%; Pred. No. 8.4e-30;
iive 46; Mismatches 87;
                                                    Query Match 27.9
Best Local Similarity 49.3
Matches 133; Conservative
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434 GLPGFISINPVHAGWLHYFVGMTISFII----AITVTLILSKRKAN
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                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuroda M., Ohta T., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Innou R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T., Hattori M.,
Ogaswara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
              VYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAKSEKL 176
                                                                                                               KGLAGASGVSAVLGITEPAIFGVŅLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGF 236
                                                                                                                                                              HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGAACLAVFFLAK-SE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMVFPSLVNGYDVAATMAAGE-MPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFL
                                                61 KRLKGTADFLITPVLTLLIGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFLGVVSIDA - - PDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51232 MW; D88607F6E0AF2E84 CRC64;
                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation updat. SUCROSE-SPECIFIC IIBC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus subsp. aureus N315.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 659; DB 2;
48.6%; Pred. No. 8.4e-30;
tive 53; Mismatches 82;
                                                                                                                                                                                                                                                                                        480 AA.
                                                                                                                                                                                                 237 LGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 266
                                                                                                                                                                                                                          434 PGIISINPQQIGYYIMGMAISFVAAFALTV 463
                                                                                                                                                                                                                                                                                    099R00 PRELIMINARY; PRT: 46
099R00, 01-JUN-2001 (TrEMBLrel. 17, Last sequen
01-JUN-2001 (TrEMBLrel. 17, Last sequen
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPOSE
SCRA OR SAZ167.
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EMBL; AP003137; BAB43469.1; -.
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Best Local Si
Matches 1399
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53 ATIEKFLHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWYGDVLAHGLQGLYDFGGP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 GCMGLFAIPSFIDPKNSMILIHFLIAIAMNFVLGFVLTQFIKIPYLYGEPTSTDSDVDDK 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AMVFPSLVNGYDV---AATMAAGEM---PMWS-LFGLDV--AQAGYQGTVLPVLVVSWIL 52
                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                Cote C.K., Cvitkovitch D., Bleiweis A.S., Honeyman A.L.;

A novel beta glucoside specific PTS locus from Streptococcus mutat that is not inhibited by glucose.";

Microbiology 146:1555-1563(2000).

R EMBL; AF206272; AAR89975-1;

R InterPro; IPR001375; PTS_EIIA.

R InterPro; IPR00335; PTS_EIIA.

R Pfam; PF00358; PTS_EIIB.

R Pfam; PF00378; PTS_EIIB.

R Pfam; PF00378; PTS_EIIS.

R Pfam; PF00378; PTS_EIIS.

R ProDom; PD00243; PTS_EIIA.;

R PROSITE; PS00371; PTS_EIIA.;

R PROSITE; PS00371; PTS_EIIA.;

R PROSITE; PS00371; PTS_EIIA.;

R PROSITE; PS00371; PTS_EIIA.;

R PROSICE 644 AA; 69282 MW; 723B7FBBDD2794EB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 PVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
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                                                                                Last sequence update)
Last annotation update)
PERMEASE.
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                                                            Created)
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                                                   01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, BETA-GLUCOSIDE-SPECIFIC EII
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                                                                                                                                                                                                 Streptococcus mutans.
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Best Local Simi
Matches 160;
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Q9KJ80
Q9KJ80;
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us-09-604-231-2.rspt

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Streptococcus pyogenes, Bacteria; Firmicutes; E
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Best Local Similarity
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                                                                                                                        SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=1314;
  OR SPY1815.
                                                                                                                                             STRAIN-SF370
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Q48408;
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Q48408
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                                                                                                                                                                                                                                                                                                                                Ferretti J.J., McShan W.M., Javic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olan Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

"Complete genome sequence of an MI strain of Streptococcus pyogenes.";

EMBL; AED06630; ARK34748.1;

"Complete proteome
SCGU U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 LHKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFG--GPVG-- 114
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                                                                                                                                                                                 Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKSEKLKG-LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 674;
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                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PTS SYSTEM ENZYME II.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II.
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                                                                                  Created)
                                        PRT;
                                                                                                                                                                                                                                                                                                     STRAIN=SF370;
MEDLINE=21192684; PubMed=11296296;
                                                                           (TrEMBLrel. 17,
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Best Local Similarity 34.49
Matches 155; Conservative
                                        PRELIMINARY;
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MEDLINE=21192684; PubMed=11296296;
MEDLINE=21192684; PubMed=11296296;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, AED06608, AAK34540.1; -.
Complete proteome.
SEQUENCE 620 AA, 65725 MW, 64F5FE83524DC4DC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAI
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Klebsiella.
NCBI_TaxID=571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CELLOBIOSE-SPECIFIC PTS PERMEASE.
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SEQUENCE FROM N.A.
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046129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 RLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLV 121
                                                                                                                                                                                                                                                                                                                                                                           122 YSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 S-----IDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLAQMIPPEGIDAT------VWGGAAGMFASLII-----ACVLTLVAG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEV 405
         Lai X., Davis F.C., Hespell R.B., Ingram L.O.; "Cloning of celloblose phosphoenolpyruvate-dependent phosphotransferase genes: functional expression in recombinant Escherichia coli and identification of a putative binding region for
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                      2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus plantarum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                      239 ILPSSMKNFFTPAICLAVVVPLTFLIIGPVATWLSQLLANGYQLIYQVAPWLAGAAMGAL
                                                                                                                                                                                                                                                                                                                                                                                                                      GASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 621;
                                                                                                                                                             Prodom; PD001476; PFS_EIEB; 1.
Prodom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA; 1.
SEQUENCE 621 AA; 65492 MW; DFIDE2A2A7B81339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                          25.9%; Score 612.5; DB 2; 32.4%; Pred. No. 4.9e-27; ive 89; Mismatches 181;
                                                    disaccharides.";
Appl. Environ. Microbiol. 63:355-363(1997)
EMBL: U61/27; AAB51563.1; -.
HSSP: P20166; IGPR.
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MEDLINE=97176370; PubMed=9023916;
                                                                                             Interpro; IPR001127; PTS_EIIA.
Interpro; IPR00196; PTS_EIIB.
Interpro; IPR003352; PTS_EIIC.
Pfam; PF00358; PTS_EIIA_1; 1.
Pfam; PF00357; PTS_EIIB; 1.
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                                                                                                                                                                                                                                                                 Conservative
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nes 154; Conserv
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Q9L461;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDPDATAAPVPAGTTKAEAEAPAEFS----NDSTIIQAPLTGEAIALSSVSDAMFASG 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHK 61
             Marasco R., Salatiallo I., De Felice M., Sacco M.;
"A physical and functional analysis of the newly identified by property of Lactobacillus plantarum.";
FEMS Microbiol. Lett. 186:269-273(2000).

EMBL; AJ25020; CAB71150.1;
InterPro; IPR001197; PTS_EIIA.
InterPro; IPR001352; PTS_EIIA.
InterPro; IPR001352; PTS_EIIB.
Pfam; PF00358; PTS_EIIB.
Pfam; PF00358; PTS_EIIB.
Pfam; PF00358; PTS_EIIB.
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                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                             Length 577;
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                                                                                                                                                                                                                                                            ProDom; PD002243; PTS_EITA; 1.
PROSITE; PS00371; PTS_EITA_1; 1.
SEQUENCE 577 AA; 60877 MW; E8C877050103B5FC CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          Score 607; DB 2; L
Pred. No. 9.2e-27;
81; Mismatches 133;
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MEDLINE-20263773; PubMed-10802183;
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MEDLINE=98151780; PubMed=9491080;
                                                                                                                                                                                                                                                                                                                                                                             25.7%;
32.6%;
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 32.6<sup>o</sup>
Matches 147; Conservative
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SEQUENCE FROM N.A.
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BH2216.
Bacillus halodurans
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                                                [1]
SEQUENCE FROM N.A.
                       NCBI_TaxID=1360;
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Q9KAS1
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                  "Isolation and characterisation of an aryl-beta-D-glucoside uptake and utilisation system (abg) from the gram-positive ruminal Clostridium species C. longisporum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKRLKGTADFLITPVLTLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 LVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKG 178
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVA--QAGYQGTVLPVLVVSWILATIEKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 KKIIPDMVKTFLVPFATLLVVVPVTFMAIGPISTIAANALGDLTLAIYNFNPTIAGLFIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 VSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGEL
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE-SPECIFIC PTS SYSTEM IIABC COMPONENT (EC 2.7.1.69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                         Brown G.D., Thomson J.A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L49336; AAC05713.1; -.
HSSP; P20166; 1GPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7D9CD1B17BE9283E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.9%; Score 589.5; DB 2;
llarity 31.2%; Pred. No. 9.8e-26;
Conservative 80; Mismatches 197;
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                                                                                                                                                                                                                                                           InterPro: IPR001127; PTS_EIIA.
InterPro: IPR001127; PTS_EIIA.
InterPro: IPR001996; PTS_EIIB.
InterPro: IPR00332; PTS_EIIC.
Pfam: PP00367; PTS_EIIB. 1.
Pfam: PP00378; PTS_EIIB. 1.
Pr0Dom; PD001476; PTS_EIIB; 1.
Pr0Dom; PD001476; PTS_EIIB; 1.
PR0SITE: PS000371; PTS_EIIA; 1.
PR0SITE: PS000371; PTS_EIIA_1; UNKNOWN_1.
SEQUENCE 616 AA; 65890 MW; 7D9CD1B17BE?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989
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                                                                                   Mol. Gen. Genet. 257:213-218(1998)
Brown G.D., Thomson J.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                         STRAIN-B6405
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Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 HKRLKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVYSPIVITGLHQSFPPIELELFNQG-GSFIFATASMANIAQGAACLAVFFLAKSEKLKG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVSIDAPDMYMFLVCAVVTFFIAFGAAIAYGL---YLVRRNGSIDPDATAAPVPAGTTKA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAEAPAEFSNDST---IIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AMVFPSLVNGYDVAATMAAGEMPMWSLFGL--DVAQAGYQGTVLPVLVVSWILATIEKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 IFSFTSNITLTGEVSGAIKIMIVSAVAVIAGFVVTYLV----GFEDDVIENPIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        636;
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01-ocr-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, TREHALOSE-SPECIFIC ENZYME II, BC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        012030D819163325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.9%; Score 588.5; DB 2; 33.5%; Pred. No. 1.2e-25; iive 76; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD002243; PTS_EIIA; 1, PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 AA.
                                                                                                       Genome Res. 0:0-0(2001).

EMBL; AE006376; AAK05558.1; -.
InterPro; IPR001343; ABC_transportr.
InterPro; IPR00135; PTS_EIIA.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR003352; PTS_EIIB.
Pfam; PF00358; PTS_EIIA.1; 1.
Pfam; PF00358; PTS_EIIE.1.
Pfam; PF00358; PTS_EIIE.1.
Pfam; PF00378; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 EFDIDAIKAAGYEVTTPIVVSN 434
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578 KFDIERIQNAGYSTQVPIIVTN
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Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KRLKGTADFLITPVLTLLITGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLAKSEKLKGL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 SLSSAVSAYLGITEPAMFGVNIRYKFPFVCAIISAAIGGAFITVNGVLANSIGVGGLPGI 434
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                         1 MAMVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGV
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                                                                                       Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                 Length 470;
                                                                                                                                                                                                                                                                                                                               24.1%; Score 569.5; DB 2; Length 42.9%; Pred. No. 9.3e-25; Live 55; Mismatches 93; Indels
                                                                                                                                                                                                                                                                    Complete proteome. - SEQUENCE 470 AA; 50185 MW; 3CE67B1E9650F5B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 AA; 66148 MW; 1AF6872CFDD7C7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE PERMEASE IIABC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 AA.
Bacillus/Staphylococcus group; Bacillus.
                                          SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                        Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
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                                                                                                                                                                           EMBL; AP001514; BAB05935.1; -. InterPro; IPR001996; PTS_EIIB. InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 VSIDAPDMVMFLVCAVVTFFI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSIQAGFWGVFFIGMVIAFIL 455
                                                                                                                                                                                                                                                                                                                                                             Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                Similarity
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SEQUENCE 620 AA;
               NCBI_TaxID=86665
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NCBI_TaxID=1314;
                                                                                                                    Horikoshi K.;
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63 LKGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDVLAHGLQGLYDFGGPVGGLLFGLVY 122
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                                                                                                                                                                                                                                                                                                                                      SIDAP----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 AEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 VAFPSGHAFAVRTKAEDGSNVDJIMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDI 416
                                                                                                                                                                                                                                                                                                    SPIVITGLHQSFPPIELELFNQGGSFIFATASMA-NIAQGAACLAVFFLAKSEKLKGLAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 QYINPSGGANFTNALIAGTATIVLAFSLTWFMG-----IDEE---SPKQVSVAADM 461
                                                                                                     3 MVFPSLVNGYDVAATMAAGEMPMWSLFGLDVAQAGYQGTVLPVLVVSWILATIEKFLHKR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 620;
23.9%; Score 564.5; DB 2; 30.8%; Pred. No. 2.5e-24; ive 93; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAIKAAGYEVTTPIVVSN 434
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DFITSKGYSLISPVVVTN 594
                                                   Conservative
                         Best Local Similarity
Matches 135; Conserv
       Query Match
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Search completed: March 21, 2002, 16:28:26 Job time: 336 sec

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(without alignments) 5163.982 Million cell updates/sec
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Sequence 17, Appl
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                                                                                                                       1 ctcatggcatctgcgccgtt......gttgaaaccttgagtgttcg 1527
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Sequence 14,
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Sequence 4, 1
Sequence 1, 1
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Sequence 43,
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                                                           March 22, 2002, 07:02:16; Search time 66.97 Seconds
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US-08-921-177-17
US-08-92-577C-17
US-08-920-828-17
US-08-673-190A-3
US-08-673-190A-6
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US-09-135-994-1
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Sequence 4, Appl:	US-08-735-609-4	~	34303	2.0	31	45	
Sequence 4, Appl:	US-08-735-609-4	~	34303	2.0	31	44	
Sequence 429, App	US-08-998-416-429	4	818	2.0	31.2	43	Ö
Sequence 196, App	US-08-905-223-196	7	342	2.0	31.2	42	
Sequence 1, Appl:	US-08-619-554-1	Н	7655	2.1	31.6	41	
Sequence 1, Appl:	US-08-928-361B-1	m	7334	2.1	31.6	40	ပ
Sequence 2, Appl:	US-08-928-361B-2	m	5511	2.1	31.6	39	ပ
Sequence 3, Appl:	US-09-074-912-3	m	1227	2.1	31.8	38	υ
Sequence 5, Appli	US-08-453-265-5	-	10366	2.1	32	37	
Sequence 5, Appli	US-08-246-982A-5	Н	10366	2.1	32	36	
	US-09-041-886-14	4	10348	2.1	32	35	
Sequence 13, Appl	US-08-556-419-13	m	10348	$^{2.1}$	32	34	
	US-08-457-273B-41	7	10348	2.1	32	33	
Seguence 3, Appl	US-08-928-361B-3	m	5318	2.1	32	32	υ
Sequence 2, Appl	US-08-700-651-2	m	5318	2.1	32	31	ပ
Seguence 4, Appl	US-08-928-361B-4	m	5163	2.1	32	30	ပ
Sequence 1, Appl	US-08-700-651-1	m	5163	2.1	32	29	ပ
Sequence 15, App.	US-08-985-916-15	4	3533	2.1	32	28	

## ALIGNMENTS

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APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Metsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: 25
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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29-AUG-1997
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                               Sequence 17, Application US/08920812
Patent No. 5763188
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
US-08-920-812-17
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
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LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
RESULT 1
US-08-920-812-17/c
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TOPOLOGY: linear
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STATE: Illinois
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Matches 540; Conserv
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APPLICANT: Ohno,
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                Length 3615;
           Score 109.6; DB 1;
Pred. No. 2.2e-23;
0; Mismatches 589;
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            Query Match 7.2'
Best Local Similarity 46.3'
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APPLICANT: Matshisa, Akio
APPLICANT: Watshisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-MUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1449 aagcgggagccaacctgctcaacgtc 1474
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; Patent No. 5770375
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Clinical Isolate EC-24
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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STRANDEDNESS: double
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                                                                                                                APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & STREET: 6300 Sears Tower, 233 South Wacker Drive
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46.3%; Pred. No. 2.2e-23;
tive 0; Mismatches 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
                                             Sequence 17, Application US/08921177
Patent No. 5798211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
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312/474-0448
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Matches 540; Conserv
                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               Illinois
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STATE: Illinoi
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STRANDEDNESS:
RESULT 3
US-08-921-177-17/c
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US-08-921-177-17
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APPLICANT: Eda, Soji TITLE OF INVENTION: Probe for Diagnosing Infectious Disease NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:

Gerstein, Murray & South Wacker Drive

ADDRESSEE: Marshall, O'Toole, Geri STREET: 6300 Sears Tower, 233 Soui CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C

19036/32420

REFERENCE/DOCKET NUMBER: 191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448

TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS: LENGTH: 3615 base pairs TYPE: nucleic acid STRANDEDNESS: double MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:

linear

APPLICATION NUMBER: US/08/362,577C FILING DATE: 27-MAR-1995 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: MAME: Rin-Laures, Li-Hsien REGISTRATION NUMBER: 33,547

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                                                                                                       Length 3615;
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                                                                                                   Score 109.6; DB 1;
Pred. No. 2.2e-23;
0; Mismatches 589;
) ORGANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-24
US-08-362-577C-17
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Best Local Similarity 46.39
Matches 540; Conservative
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Sequence 17, Application US/08362577C Patent No. 5807673 GENERAL INFORMATION: APPLICANT: Ohno, Tsuneya

US-08-362-577C-17/c

APPLICANT: Ohno, Tsuneya APPLICANT: Matsuhisa, Akio

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                            1075 CCTGTATCAGTGGGGCTTTGGGGGCCCACCATTATTGGCTACGCGCAAACGAAGTCTACT
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APPLICANT: Matsuhisa, Akio
APPLICANT: Welara, Hirotsugu
APPLICANT: Bda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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Patent No. 5853998
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Il
COUNTRY:
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Pred. No. 2.2e-23;
0; Mismatches 589;
                                                                                                       Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19036/32420
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-ENTIN RELEASE #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/920,828 FILING DATE: 29-AUG-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                  FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION NOTA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rin-Laures, Li-Hslen
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
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LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 312/474-0448
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Best Local Similarity 46.3
Matches 540; Conservative
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US-08-920-828-17
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1955 TCACCGTCTGGGCCAGCGTTATTGGCGGTGTCATTGCCATCGGTTGCGCATTTGTCGGTA 1896
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                                                                                                                                                             -----GAAGAGAAAACACCAGAGGTTATTACACCACCTGAGCAGGGGGGTA 1798
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                                       tttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgcctg
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STREET: 1300 I Street, N.W., Suite 700
                                                                             1895 CGGTGATGCTTCATTTCATCACGCTAAACGTCAGCCAGCGCAGGGTGCCCC
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Stegmaier, Sabine
APPLICANT: Stegmaier, Sabine
APPLICANT: Stegmaier, Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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NAME: Forman, David S.
REGISTATION VIMBER: 33,694
REFERENCE/DOCKET NUMBER: 06473.0001-00000
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TORNEY AGENT TWO
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Patent No. 5985668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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ZIP: 20005-3315
COMPUTER READABLE FORM:
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US-08-673-190A-3/c
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Data I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                      Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                      Score 97.8; DB 2;
Pred. No. 2.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Stegmaier, Sabine
APPLICANT: Stegmaier, Sabine
APPLICANT: Stegmaier, Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ANDRESS:
                                                                                                                                                                                                                                                                                                                                                      Score 97.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/673,190A FILLING DATE: 27-JUN-1996
                                                                                                                                                                                                                                                         Protaminobacter rubrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08673190A
Patent No. 5985668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 gccaattgagctggagctgtt 525
                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Protaminobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
TELEPHONE: (202)408-4000
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                      6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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                                                                                                      LENGTH: 465 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 Matches 204; Conservative
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                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                         linear
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                              US-08-673-190A-3
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FILING DATE:
APPLICATION NUMBER:
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Best Local Similarity 53.1%; Pred. No. 2.4e-12;
Matches 152; Conservative 0; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 atttcggtggtccagtcggcggtctgctcttcggtctggtctactc 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08232463
Patent No. 5570367
CENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
TILLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardher
STREET: 1800 Diagonal Road, Suite 500
CITY: ALexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                 33,694
ER: 06473.0001-00000
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APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/232,46:
                                                                                                                                                                                                                                                                                                   Enterobacter species
       ATTORNEY/AGENT INFO 1730

ATTORNEY/AGENT INFO 1730

REGISTRATION NUMBER: 33,694

REFERENCE/DOCKET NUMBER: 0647

TELECOMMUNICATION INFORMATION:
TELEFRAN: (202)408-4400

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati)
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                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                 ; ORGANISM:
US-08-673-190A-6
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147 ccaccatggctgcgggcgaaatgccaatgtggtccctgtttggtttagatgttgcccaag 206
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: PLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VERBER, Claire M.
APPLICANT: VERBER, JOHn C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-220007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 ccggttaccagggcaccgtgcttcctgtgctggtggtttcttggattctggcaacgatcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 gcgatgtgctggcacacggtctacagggactttatgatttcggtggtccagtcggcggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 tgctcttcggtctggtctactcaccaatcgtcatcactggtctgcaccagtccttcccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgttgctgctcaccggattccttacattcatcgccattggcccagcaatgcgctgggtgg
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                                                                                                      REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                            29,768
                                                                                                                                                                                                          TELEX: 899149 INFORMATION FOR SEQ ID NO: 14:
                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                          26-AUG-1991
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                              ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-840A-2/C
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3923099 CCGACGGTGCCGTGGCGCGTTACCGCCGTCACCGCCGTTGCCGCCGTTGCCGCCGTTG 3923040
                                                                                                                                                                OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747 tcggtggcgctttgattgcactctttaatatcaaggcagttgcgttgggcgctgcaggtt 806
                                                                                                                                                                                                                                                                                                                                                                                                      627 tcaagggccttgcaggtgcttcaggtgtctccgctgttcttggtattacggagcctgcga 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    867 ttaccttcttcatcgcattcggcgcagcgattgcttatggcctttacttggttcgccgca 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927 acggcagcattgatccagatgcaaccgctgctccagtgcctgcaggaacgaccaaagccg 986
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                               DB 4; Length 4403765;
                                                                                                                                                                                                                                                                                                       Score 37.2; DB 4; Length 4 Pred. No. 18; 0; Mismatches 213; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-417-119A-1/C
Sequence 1, Application US/08471119A
Sequence 1, Application US/08471119A
Sequence 1, Application US/08471119A
Setent No. 582770S
Sequence 1, Application US/08471119A
APPLICANT: Leituer, Ernst
APPLICANT: Schoeider, Elisabeth
APPLICANT: Schoeider, Elisabeth
APPLICANT: Schoeider, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
STREET: 59 Route 10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 3922919 AAGTCGCCGGAGCCGCC 3922902
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Best Local Similarity 43.7%;
Matches 165; Conservative
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COMPUTER READABLE FORM:
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29376 CGATACGGCGCTCTGAGCTCGCTGGAGTGGCCGGTTCGTCAGGGTTCGAAGTTGTCGAC 29317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 46899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reeders, Stephen
APPLICANT: Schneider, Michael
APPLICANT: Glucksmann, Sandra
TITLE OF INVENTION: IDENTIFICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,751 FILING DATE: US-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                       100-8029/CONT/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.6;
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 7638-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Tolypocladium niveum STRAIN: ATCC 34921
US-08-471-119A-1
                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8677
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08460751 Patent No. 5891628 GENERAL INFORMATION:
NAME: Kassenoff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100
                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 03-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 55.49
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSE: Pennie &
                                                                                                                                                                                                                                      unknown
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Av
CITY: New York
                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE:
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LENGTH: 14060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
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APPLICANT: Baltz,
APPLICANT: Brought
                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-658-136-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-036-987A-1
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6939 CAGCGCACACCCGCCAGCCTCCTGTGTCGAAGCCACACAGGCCCCAGTGGAAACTGAG 6880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 cactgcagacttcctgatcactccagtgctgacgttgctgctcaccggattccttacatt 354
                                                                                                                                                                                                                                                                                                                                                                                                        235 gctggtggtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaaggg 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 catcgccattggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacaggg
                                                                                                                                                                                                                                                                                                                              2.1%; Score 32.8; DB 2;. Length 12912; 48.9%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: LANDES, TIMOTHY D
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGIESTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/658,136 FILING DATE:
              TELEPHONE: (212) 790-9090
TELESAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12912 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENZYME CORPORATION
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 88; Conservative
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STATE: MASSACHUSETTS
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                                                                                                                                                                           unknown
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                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-460-751-1
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US-08-658-136-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                   295 cactgoagacttcctgatcactccagtgctgacgttgctgctcaccggattccttacatt 354
                                                                                                                                                                                                     235 gctggtggtttcttggattctggcaacgatcgagaagttcctgcacaagcgactcaaggg 294
                                                                                                                                                                                                                                                                                                                                                                                        355 catcgccattggcccagcaatgcgctgggtgggcgatgtgctggcacacggtctacaggg 414
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                                                                                                                Length 14060;
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APPLICANT: Ranum et al.
TITLE OF INVENTION: SCAT GENE AND METHODS OF USE
TITLE OF INVENTION: SCAT, of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SCOTUMER PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 32.6; DB 4;
60.9%; Pred. No. 2.5;
tive 0; Mismatches 34;
                                                                                                                DB 3;
                                                                                                                                                           0; Mismatches
                                                                                                                                     Pred. No. 16;
                                                                                                                Score 32.8;
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Crawford, Kathryn P.
Maddurl, Krishnamurthy
Merlo, Donald J.
Treadway, Patti J.
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                                                                                                             2.1%;
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Matches 88; Conservative
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Matches 53; Conservative
CDS
135..13040
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ORGANISM: Homo sapiens
US-09-135-994-1
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LENGTH: 80.
TYPE: DNA
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APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVERTION: Blosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Baltz, Richard H
APPLICANT: Baltz, Richard H
APPLICANT: Crawford, Kathryn P
APPLICANT: Maddwit, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
APPLICANT: Turner, Jan R
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                         STREE: Dow AgroSciences LLC Patent Department STREE: 9330 Zionsville Road CITY: Indianapolis STRE: Indianapolis
                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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Pred. No. 52;
0; Mismatches
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CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
BARLIER FILING DATE: 1998-03-09
                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/09/036,987A
09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
REFERENCE/DOCKET NUMBER: 50,6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09370700 Patent No. 6274350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%;
Best Local Similarity 53.5%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 80161 base pairs
nucleic acid
DEDNESS: double
                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agros
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                                                                                                                                                                                                Indiana
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                                                                                                                                                                                                                                           46268
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-036-987A-1
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                                                                                                                                                                                                                                                      61 cgtttcggcggcaatgagttcctgggcgccgcgtattggtatggcgatggtgttcccgag 120
                                                                                                                                                                                                                ő
                                                                                                                                                                          DB 4; Length 80161;
                                                                                                                                                                      Score 32.6; DB Pred. No. 52; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 22, 2002, 09:23:24 Job time: 8468 sec
                                                                                            ORGANISM: Saccharopolyspora spinosa US-09-370-700-1
                                                                                                                                                                          2.1%;
                                                                                                                                                                                                                Conservative
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver.
SEQ ID NO 1
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            14756 cacggtt 14762
                                                                                                                                                                                                                                                                                                                                                                                                        cctgttt 187
                                                      80161
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Drosophil 1000055A0

ALO67821 AM583970 ALO31881 ALO97099 ALO97099 ALO877921 ALIB1976 AM573719 BES98387

Tetraodon

wt46c03.x EST391869

AI982977

EST391888

AW980716 BW980735 BG581619 BG581892 BG582423 BG583630 BG584630 BG584640 BG5

Title: Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

0B 0B

Minimum Maximum

Database

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticaee; Hordeum.

E. 1 (Lases 1 to 680)

Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.

EST sequencing and analysis in barley

L. Unpublished (2000)

Contact: Michalek W

Institute for Plant Genetics and Crop Plant Research

Corrensstr.3, D-06466 Gatersleben, Germany

Email: michalekeipk-gatersleben, dermany

Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL506562 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY02I24T 5', mRNA sequence.
AL506262 GI:12032477
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/cultivar="Barke"
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/clone="HY01214T"
/clone=Lib="Hordeum vulgare Barke developing caryopsis
(3.-15.DAP)"
/tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                            CNS0021D
BF727921
CNS025EN
AW573719
BE998387
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BE721200
CNS03HA0
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BG581619
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BG583630
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BI118076
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AI917973
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AI499080
BE158004
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AL193990 Tetraodon
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100
Listing first 45
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em_gss_rod:*
em_gss_vrt:*
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/note="Vector: plasmid pBk-CMV; Site\_1: EcoRI; Site\_2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting

EST429681 EST316674 EST482254 EST430136

AW574083 BG580528 BE998413 B

Tetraodon Tetraodon

AL065923 AL238306 AL078875 AL243904

BE998413 CNSO06U0 CNSO3CVD CNSO0LXJ CNSO3H6V

BE997958 AW574083

Score

Result o N

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BG580528

468.8 411.8 411.6 411.4 411.4 411.4 400.8 400.8

Drosophi

Drosophil

AL071370 Drosophil A1318021 SWOVAFCAP BE721200 188296 MA AL244017 Tetraodon

AW173566 xj08h03.x AI917973 tz16d08.x

AW440291 PAI499080 1 BE158004 PAI

Tetraodon

AW516253 A AI564728 A AL196412 A AZ982613

602867346 Drosophil

605087H03

AI812147 BI118076

us-09-604-231-1.rst

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Unpublished
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variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5' and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Steven, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M.

Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 cettgcaggtgettcaggtgtctccgctgttct---tggtattacggagcctgcgatctt 690
                                                                                                                                                                                                                                                                              caccytycttcctytyctygtyttcttygattctygcaacyatcyagaagttcctyca 279
                                                                                                                                                                                                                                                                                                                551 CACGGTGATCCCGGCGCTGGTGATGACCTGGTGCCTGTCATATATCGAACGCTGGGTGGA 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 cgcccagggtgcggcatgtttggcagtgttcttcctggcgaagagtgaaaagctcaaggg
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                                                                                                                                                                                                              Length 680;
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                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                         Score 48.8; DB Pred. No. 0.03; 0; Mismatches 2
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/organism="Homo sapiens"
/db_xref="ATCC (inhost):86662"
/db_xref="ATCC (inhost):86662"
/db_xref="Cano:9060"
/db_xref="Cano:9060"
/clone="FB20C8"
/clone="FB20C8"
/clone="FB20C8"
/clone="Cano: January (catalog #97720), Stratagene) was constructed by directional cloning and ollyo d(7)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
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1 (bases 1 to 681)
1 (bases 1 to 681)
1 Neost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Boune
Bernot, A., Fizames, C., Wincker, P., Brottler, P.,
Saurin, W. and Weissenbach, J.
                                                                                           Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 30327008637
Fax: 3032707097
Email: nikki@tally.uchsc.edu.
Nature Genet. 2, 180-185 (1992)
94258200
On Sep 21, 1992 this sequence version replaced
Contact: Sikela JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Genoscope.
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Direct Submission
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-and sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                            ID : COAG262DD07LP1~end : T7" t 50 others
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Pterygota; Neoptera; Endopterygota; Diptera; Erachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 895)
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Corganism-Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="262H14"
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40.9%; Pred. No. 2.2;
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AL066286
AL066286.1 GI:4945153
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ESTs from senescent nodules of Medicago truncatula
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; on bw ap, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hypridization from the BACPAC Resource Center can be location/Qualifiers
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University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
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clone
                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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EST429681
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/cultivar="genotype Al]"
/db_xxef="taxon:3880"
/clone_"bgNN-51G2"
/clone_"bgNN-51G2"
/clone_lib="GVN"
/tissue_type="N2-fixing root nodules harvested one month dev_actage="Effective root nodules harvested one month post inoculation with Sinorhizoblum meillot!"
/lab_host="E. coll strain XLOLR"
/lab_host="E. coll strain XLOLR"
/lab_host="E. coll strain machen meillot!"
/lab_host = "Coll strain machen meillot!"
/lab_host = "E. coll strain machen meillot!"
/lab_host = "Coll strain machen meillot!"
/ Anot: cDNA was prepared from poly+ enriched RNA from effective root nodules harvested one month post incollation with Sinorhizoblum meillot!. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                  Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
Thil Borlaud Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
TT-1: 612 625 515
Fax: 651-649-5058
                                                                                                                                                                                                                Minnesota EST name:M252981e
TIGR sequence name:MTCAR37TK
More information is available at.
'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
                                                                                                                                                                                       Email: vance004@maroon.tc.umn.edu
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Contact: Carroll P. Vance
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Best Local Similarity 50.2%;
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                           /tissue_rype="senescent root nodules"
/tissue_rype="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/note="vector: pBluescript SK +/-; Site_1: EcoRI; Site_2:
xhoī; cDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
at mid-pod stage. The
collected from 2 month old plants at mid-pod stage. The
collected from 2 month old plants at mid-pod stage. The
collected from 2 month old plants at mid-pod stage. The
collected from 2 month old plants at mid-pod stage. The
packaging extracts. Plasmids containing cDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist hadge and propagated in SOLR cells."
37 a 100 c 101 g 139 t
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Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,J.E. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
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Medicago truncatula
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Megnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST316674 GVN Medicago truncatula cDNA clone pGVN-51G2, mRNA
                                               University of Minnesota name: M271936e TIGR sequence name: MTKAROSTKB More information is available at: http://chrysie.tamu.edu/medicago Seq primer: SKMOG (CTA 9AA CTA 9tg 9AT CC).
Location/Qualifiers
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                                                                                                                                                                                                                /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                         Email: vance004@maroon.tc.umn.edu
                                                                                                                                                                                                                                                                                              /clone="pGVSN-8B9"
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AW574083.1 GI:7238816
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50.28;
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Matches 102; Conservative
  Fax: 651-649-5058
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BG580528 601 bp mRNA EST 11-APR-2001
EST482254 GVN Medicago truncatula cDNA clone pGVN-57H8 5' end, mRNA
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                                                                            Gaps
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Length 559;
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Score 41.4; DB 10;
Pred. No. 2.7;
0; Mismatches 101;
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WAND ALLERANCE

TITLE

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eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="medicago truncatula"
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/clone_lib="GVSN"
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                                                                                                                                  Unpublished (2000)
Contact: Carroll P. Vance
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                                              (bases 1 to 627)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="pGWN-5780"
/clone=lib="GWN"-5780"
/clone=lib="GWN"-5780"
/clone=lib="GWN"-5780"
/clone=lib="GWN"-fixing root nodules harvested one month post inoculation with Sinorhizoblum mellioti"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from poly4+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizoblum mellioti. The cDNA-was directionally ligated into the Uni-2AP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells:"
                                                                                                                                                                                                                                                          Email: varce0040maroon.tc.umn.edu
University of Minnesota name: M381580e TIGR sequence name:
MTCCT40TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                    Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M. ESTs from one month old nitrogen-fixing root nodules of Medicago
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                          truncatula, 2001
Unpublished (2001)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
University of Minnesota
Til Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Fax: 651-649-5058
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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1 (bases 1 to 601)
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/issue__rype="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-; Site_1: BcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP KR vector from Stratagene and packaged using Gigapack III Gold packaging extracts; Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using excised from the recombinant lambda-ZAP phage using ex-Assist helper phage and propagated in SOLR cells."
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Fedorova, M., Pierson, B.L., Samac, D.A., Gantt, J.S., Vance, C.P., Town, C.D., Bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.
ESTs from senescent nodules of Medicago truncatula
                                                                                                                                                                                Department of Agronomy and Plant Genetics
University of Minnesota
Table 512 625 5715
Fax: 651-649-5058
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N12 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL065923
AL065923.1 GI:4944891
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                                                                                                                                                                                                                                                                                                                                                                            Email: variee004@maroon.tc.umn.edu
University of Minnesota name: M772391e TIGR sequence name:
WRAF954K More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N21"
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RESULT 10 CNS03CVD/c

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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                       survey sequence PUC-Ori end of clone
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                          Fisher, C.,
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR48E16 of RPCI-98 library from Drosophila melanogaster (fruit
                    Tetraodon nigroviridis genome survey sequence PUC-Or1 ena or cado 015b07 of library G from Tetraodon nigroviridis, genomic survey
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="015D07"
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Tetraodon nigroviridis
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Best Local Similarity 53.0%;
Matches 87; Conservative (
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                                                                                                                                    Lubert Submission of the Sequence of E-mail is seqref@genoscope.cns.fr.

- Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCF is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitily.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRd ingestion of Drosophila DNA provided by the BDCP from the isogenic strain y2: cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
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tive 96; Mismatches 147;
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/clone="BACR48E16"
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Tetraodontidae; Tetraodontidae; Tetraodon.

1 (bases 1 to 970)

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Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
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15 others
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Location/Qualifiers
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/db_xref="taxon:99883"
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Pred. No. 6.5;
2; Mismatches 151;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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/clone_11b="G"
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VERSION
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Direct Submission

Learn Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EWRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuchoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; co bw spy, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Drosophila melanogaster genome survey sequence T7 end of BAC: BACR23F02 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. AL067821
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/db_xref="taxon:7227"
/clone=lib="RPCI-98"
/clone="BACR23F02"
/note="end : T7"
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48.4%; Pred. No. 12;
tive 1; Mismatches 110;
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/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/lote="vector: pBluescript SN +/-; Site_1: EcoRI; Site_2:
xhoi; cDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage. The
cDNA was directionally ligated into the Uni 2AP XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                              Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Town,C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTs from senescent nodules of Medicago truncatula
                                                                                     Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                       Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlauq Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
7el: 612 625 5715
Fax: 651-649-5058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M271935e TIGR sequence name:
WTKAKOSTK More information is available at:
http://chrysie.tamu.edu/madicago
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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/cultivar="genotype Al7"
/db_xref="taxon:3880"
/clone="pgvsN-8B9"
/clone_lib="gvsN"
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                                                                Medicago truncatula
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Carroll P. Vance
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/dev_stage="adult"
//dev_stage="adult"
//dev_s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Eye library. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LiML (info@image.llnl.gov). IMAGE ID=1785384 The following repetitive elements were found in this cDNA sequence: Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which 3' ESTs had been derived were used as a driver in a hybridization with the normalized whole-eye library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                  1 (bases 1 to 539)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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/strain="Sprague-Dawley"
/db_xref="texon:10116"
/clone="UI-R-Y0"
/clone="UI-R-Y0"
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ilarity 51.1%; Pred. No. 13;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-113-944-1

US-09-135-994-1

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US-08-108-955A-9

US-08-985-916-15

US-08-985-916-15

US-08-928-361B-3

US-08-928-361B-3

US-08-457-273B-41

US-08-457-419-13

US-08-46-982A-5

US-08-46-982A-5

US-08-46-982A-5

US-08-46-982A-5

US-08-46-982A-5

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US-08-921-177-17
US-08-32-577C-17
US-08-320-928-17
US-08-232-463-13
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3-08-363-255-1
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    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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## ALIGNMENTS

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Sequence 17, Application US/08920812
Sequence 17, Application US/08920812
Patent No. 5763188.
GENERAL INFORMATION:
PAPLICANT: Union, Tsuneya
APPLICANT: Uehara, Hirotsugu
APPLICANT: Uhinois
CONRTRE: Chicago
CITY: Chicago
STATE: Inhois
COMPUTER: United States of America
ZIF: 60606-6402
COMPUTER: EMADABLE FORM:
MEDIUM TPE: Floppy disk
COMPUTER: Paperent Release #1.0, Version #1.25
COMPUTER: Paperent Release #1.0, Version #1.25
COMPUTER: 29-ANG-1997
COMPUTER: 27-ANG-1997
APPLICATION NUMBER: US/08/920,812
FILING DATE: 27-ANG-1995
ATONNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/932420
TELECOMMUNICATION INFORMATION:
REDERENCE/DOCKET NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 33,547
REDERENCE/DOCKET NUMBER: 33,547
REPERENCE/DOCKET NUMBER: Genomic DNA
ORGANIAL SOURCE: Genomic DNA
ORGANIAL SOURCE: Genomic DNA
ORGANIAL SOURCE: CHARACTERIAL S
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                 LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
312/474-6300
312/474-0448
                              TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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 TELEPHONE:
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                  Length 3615;
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6300 Sears Tower, 233 South Wacker Drive
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                              6.4e-19;
                  DB 1;
                                                0; Mismatches
              Score 91;
Pred. No. (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE
OMPOTER: PLOPSY SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/08920827
Patent No. 5770375
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Webara, Hirotsugu
APPLICANT: Uehara, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagn
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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FILING DATE: 29-AUG-1997
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REGISTRATION NUMBER: 33,547
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                8.2%;
53.7%;
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                             Similarity 53.7
40; Conservative
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CLASSIFICATION:
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6300 Sears Tower, 233 South Wacker Drive
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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Patent No. 5798211
GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Watsuhisa, Akio
APPLICANT: Uchara Hirotsugu
APPLICANT: Eda, SOji
TILLE OF INVENTION: Probe for Diagn
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                              ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
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ropology:
                                          APPLICANT:
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53.7%; Pred. No. 6.4e-19;
tive 0; Mismatches 195; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                          NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERNCE/DOCKET NUMBER: 19036/32420
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-WAR-1995
ATTORNEY/AGENT INFORMATION:
                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/921,177
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
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US-08-362-577C-17/C
'Sequence 17, Application US/08362577C
'Patent No. 5807673
'CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-24
US-08-921-177-17
                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
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Best Local Similarity 53.74
Matches 240; Conservative
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1738 GCCAGTGGCCTGTTGGGTAAAGGTATTGCCATTCTGCCCTCGGTTGGTGAAGTGCGTTCT 1679
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                                                                                  APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
                                                                                                                                                                                           3: Marshall, O'Toole, Gerstein, Murray 6 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
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27-MAR-1995
11.: 536
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                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; STRAIN: Clinical Isolate EC-24
US-08-362-577C-17
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REGISTRATION NUMBER: 33,547
REFREENCE/DOCKET NUMBER: 1903
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                        Uehara, Hirotsugu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 36.15 base pairs
                               Matsuhisa, Akio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 27-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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Ohno, Tsuneya
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                                                                                                                                     NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
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STRANDEDNESS:
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970 attgttgtttcgaattacaagaaaaccggacctgtaaacacttacggtttgggcgaaatt 1029
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                          790 aaggetgaggatggttecaatgtggatatettgatgeacattggtttegacacagtaaae 849
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                                                                                                                       850 ctcaacggcacgcactttaacccgctgaagaagcagggcgatgaagtcaaagcaggggag
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CITY: Washington
STATE: D.C.
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US/08/673,190A
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
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62.6%; Pred. No. 0.0048;
tive 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mattes, Ralf
APPLICANT: Klein, Kathrin
APPLICANT: Stegmaier, Sabine
TITLE OF INVENTION: Sucrose Metabolism Mutants.
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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NAME: FORMAN, David S.
REGISTATION UNBER: 33.694
REFERENCE/DOCKET UNBER: 0647:
TELECOMMUNICATION INFORMATION:
TELEFAN: (202)408-4000
TELEFAX: (202)408-4000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity 62.6%
Matches 62; Conservative
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1738 GCCAGTGGCCTGTTGGGTAAAGGTATTGCCATTCTGCCCTCGGTTGGTGAAGTGCGTTCT 1679
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                                                                                                                                                                                                                                                                                                                                                                                 Probe for Diagnosing Infectious Disease
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                                                                                                                                                                                                                                                                                    APPLICANT: Ohno, Tsuneya
APPLICANT: Matsubisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Ga, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disea
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: ADDRESSE: ANDRESSEE: AMESHAll, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.2%; Score 91; DB 2; Length 361
Best Local Similarity 53.7%; Pred. No. 6.4e-19;
Matches 240; Conservative 0; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19036/32420 TELECOMMUNICATION INFORMATION:
                                              1030 gaagegggagecaacetgeteaaegte 1056
                                                                                          1390 AGCGCAGGTGAACCGCTGTTATCCATC 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                             Sequence 17, Application US/08920828
Patent No. 5853998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: line
MOLECULE TYPE: G
ORIGINAL SOURCE:
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                                                                                                                                                                 SULT 5
-08-920-828-17/c
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LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION A35
FILING APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.7
FILING DATE:
APPLICATION NUMBER: 25 - ANG-1991
ATORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMULCATION INFORMATION:
TELEFANGE (703)836-9300
TELEFAN: (703)883-4109
                                                                         69 tctgcaccagtccttcccgccaattgagctggagctgtt 107
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                           99 CATICACCACAGCTICCACGCCGIAGAGGGGGGGGCTGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: ACCEPTANT FOR THE TOTAL OF THE TOTAL
                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
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IMMEDIATE SOURCE:
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Db 3923279 TTACCGCCGTCGCCGCTGCCCCCGTCGCCGATGCCCTGGCTGCCAGCGTTACCG 3923220
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                    209 tcaagggccttgcaggtgcttcaggtgtctccgctgttcttggtattacggagcctgcga 268
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436 gtgtgtgcagttgttaccttcttcatcgcattcggcgcagcgattgcttatggcctttac 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FRASER, Claime M.
APPLICANT: FRASER, Claime M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                   Length 4403765;
                                                                                                                  496 ttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgcct 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09103840A Patent No. 6294328
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APPLICANT: FLEISCHMAN, Robert D.
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Best Local Similarity 43.77
Matches 165; Conservative
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509 acggcagcattgatccagatgcaaccgctgctccagtgcctgcaggaacgaccaaagccg 568
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                                                                                                                                                                                                          Query Match 2.9%; Score 32.4; DB 4; Length 292; Best Local Similarity 58.2%; Pred. No. 0.85; Matches 57; Conservative 0; Mismatches 41; Indels
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISCRATION NUMBER: 29,768
REGISCRATION NUMBER: 29,768
REGISCRATION NUMBER: 29,768
REGISCRATION NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703)683-4109
                                                                   /product= "sAFPB (S6)"
/note= "skin-type antifreeze
polypeptide 8 (sAFPB)"
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ITILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 32.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7218 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
                     NAME/KEY: CDS
LOCATION: 36.200
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                       US-09-117-121-29
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Patent No. 6307020

GENERAL INFORMATION:

APPLICANT: Hew, Choy

TITLE OF INVENTION: and Nucleic Acids

TITLE OF INVENTION: and Nucleic Acids

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STREET: Confifernia
                                                                                                                                                                                                                                                                                                                                                                                                  Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
ATTORNEY AGENT INFORMATION:
NAME: Weber: Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/POCKET NUMBER: 31,677
REFERENCE/POCKET NUMBER: 31,677
REFERENCE/POCKET NUMBER: 31,677
                APPLICANT: Ranum et al.

TITLE OF INVENTION: SCA7 GENE AND METHODS OF USE
FILE REFERENCE: University of Minnesota
CURRENT APPLICATION NUMBER: US/09/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 60/056,170
BARLIER APPLICATION NUMBER: 60/056,170
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 15 SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                             Score 32.6; DB 4;
Pred. No. 0.98;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 aaagccgaagcagaagcacccgcagaa 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 gcagcagcagcagcagcagcagca 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.9%;
Best Local Similarity 60.9%;
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 292 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-09-135-994-1
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GENERAL INFORMATION:
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643 TGATTTTTCGGTGTACGAATCGGAATCAGAAGATCCCATCACCATGCTTTCCAG 588

489 cetttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgctccag

763 TGCGGGAGTTGATGCCGGTTTCATTAATGCCATTGTAGTAGTTGCTGAAGATGTGGGCTT 704

APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSH TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE

P.C.

3: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTAD 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:

ADDRESSEE:

CITY: ARLINGTON

COUNTRY:

COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPILGATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435

Floppy disk

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:

NAME: NORMAN F. OBLON
REGISSTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000

TELEPHONE: 703-220 SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: double

linear

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Sequence 15, Application US/08985916
Patent No. 6221636
GENERAL INFORMATION:
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US-08-985-916-15
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                                                                                                                          gacacagtaaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatgaagtc 897
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 Best Local Similarity 2.2%; Pred. No. 6.6;
Matches 7; Conservative 177; Mismatches 135; Indels
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VENTION: No. 6187580el Pectate Lyases
NCE: 5378.200-US
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PRIOR PELLING DATE: 1997-11-24
PRIOR PELLING DATE: 1997-11-24
PRIOR FILING DATE: 1997-12-02
PRIOR PELLING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 60/067,240
PRIOR PLILING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 09/073,684
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 09/184,217
PRIOR FILING DATE: 1998-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09198955A Patent No. 6187580
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Glad, Sanne O. S.
Kauppinen, Markus S.
Schnorr, Kirk
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Schulein, Martin
Lange, Niels E.
Bjornvad, Mads E.
2.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Bacillus
US-09-198-955A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-198-955A-9/C
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                                                                                                                                                          DB 4; Length 3533;
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                                                                                                                                                        Score 32; DB 4
Pred. No. 5;
0; Mismatches
                                Brevibacterium lactofermentum
                                                                                                                                                          2.9%;
48.9%;
                                                                                                                                           Query Match
Best Local Similarity 48.5.
These 86; Conservative
                                                                        ; NAME/KEY: CDS
; LOCATION: 321..3077
US-08-985-916-15
                                               STRAIN: ATCC 13869
MOLECULE TYPE: 9
                                ORGANISM:
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Gaps

90; Indels

0; Mismatches

Best Local Similarity 48.9 Matches 86; Conservative

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369 tgcgttgggcgctgcaggttcttgggtgttgttctattgatgctccagatatggtcat 428

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Search completed: March 22, 2002, 09:48:25 Job time: 9969 sec
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                                                                                                                                                    GENERAL INCORMATION:
APPLICANT: PETERSEN CAROLYN
APPLICANT: PETERSEN CAROLYN
APPLICANT: HEESTH, AMES
APPLICANT: HEESTH, AMES
APPLICANT: HEESTH, AMES
APPLICANT: HEESTH, AND RICHARD, C.
APPLICANT: HEESTH, AND TRANCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: TWECTIONS
TITLE OF INVENTION: TWECTIONS
TITLE OF INVENTION: TWECTIONS
TITLE OF INVENTION: 10FC710NS
THERE REPREMENT: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 1
LENGTH: 5163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petersen, Carolyn VERWION: PEPTIDES, GLYCOPROTEINS, VERWION: THEIR FUNCTIONAL MOTANTS, VARIANTS, ANALOGS AND FRAGMENTS VERWION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM VENTION: SPECIES INFECTIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 gcaggtttcttgggtgttgtttctattgatgctccagatatggtcatgttcttggtgtgt 441
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3136 GGGAATAAGGTTCACCTGGGTTCTCAAACGGCAAAGGAACATTTTCCACATGGCAT 3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 5163;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 32; DB Best Local Similarity 53.1%; Pred. No. 6.3; Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
                                                                                                               Sequence 1, Application US/08700651B Patent No. 6015882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-928-361B-4/c
; Sequence 4, Application US/08928361B
; Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Cryptosporidium parvum
US-08-700-651-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: Peters
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                                                                 RESULT 14
US-08-700-651-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
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322 gcagctatcggtggcgctttgattgcactctttaatatcaaggcagttgcgttgggcgct 381
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                                                                                                                                                                                                                                                                                                                                             Length 5163;
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                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                           Score 32; DB 3
Pred. No. 6.3;
0; Mismatches
                                                                   REGISTRATION NUMBER: 30,518
REPREMENCE/POCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 us 60/026,062
                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-928-361B-4
                                                                                                                             TELEFAX: 650-324-20...

TELEFAX: 650-324-20...

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5163 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                             2.9%;
53.1%;
APPLICATION NUMBER: US 6(FILING DATE: 13-SEP-1996 ATTORNEY/AGENT INFORMATION: NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                           Ouery Match 2.99
Best Local Similarity 53.19
Matches 68; Conservative
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March 22, 2002, 08:53:35 ; Search time 157.11 Seconds
(without alignments)
6051.643 Million cell updates/sec
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1 tatgatttcggcggtccagt......gttgaaaccttgagtgttcg 1109
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/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:\*/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:\*

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29	99	65.2	59.5	59.2	59.2	54.2	53.2	53.2	53.2	51.8	51.4	51.4	51	49.2	46	45	44.6	44.2	43.2	43	42.8	42	41.6	-	40	39.8		38.6			37.2		37.2
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## ALIGNMENTS

Schroeder H, Zelder O, Haberhauer G; Phosphoenolpyruvate; sugar phosphotransferase system; PTS; ds. C.glutamicum phosphoenolpyruvate DNA #2. BP. 99US-0142691.. 99US-0150310. 99DE-1042095. 99DE-1042097. AAF31529 standard; DNA; 1109 27-JUN-2000; 2000WO-IB00973 Corynebacterium glutamicum. 09-APR-2001 (first entry) Pompejus M, Kroeger B, WPI; 2001-080989/09 (BADI ) BASF AG. WO200102583-A2 01-JUL-1999; 23-AUG-1999; 03-SEP-1999; 03-SEP-1999; 11-JAN-2001. AAF31529; AAF31529 RESULT 

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers

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Sequence 1527 BP; 304 A; 392 C; 430 G; 401 T; 0 other;
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                             present invention relates to Corynebacteium glutamicum
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tive 0; Mismatches
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation -
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium as saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           part of the printed directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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07-APR-2000; 2000JP-0159162.
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Oy Dp	301	<pre>ttcttcatcggtatcggtaccgcagctatcggtggcgctttgattgcactctttaatatc 3                                     </pre>	360 110550
Qy	361 110549	<pre>aaggcagttgcgttgggcgctgcaggtttcttgggtgtttttttt</pre>	420 110490
QY	421	<pre>atggtcatgttcttggtgtgtgcagttgttaccttcttcatcgcattcggcgcaggatt 4                                    </pre>	480 110430
Qy Dp	481	gcttatggcctttacttggttcgccgcaacggcagcattgatccagatgcaaccgctgct 5	540 110370
Qy	541 110369	ccagtycctycaygaacyaccaaayccyaaycayaaycacccycayaatttcaaacyat 6	500 110310
Qy Db	601 110309	tccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcgtcagcgat 6	560 110250
QV	661 110249	gccatgtttgccagcggaaagcttggctcgggcgttgccatcgtcccaaccaa	720 10190
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Qy	841 110069	acagtaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatgaagtcaaa 9	10010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Senoh A, Ikeda M, Ozaki A;
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99.9%; Pred. No. 0;
1ive 0; Mismatches 1; Indels 0; 0
                                                                                                 amino acid synthesis; vitamin; saccharide;
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                                                                 C glutamicum coding sequence fragment SEQ ID NO: 2904.
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The present sequence encodes the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate:sugar transport system) enzyme II. which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.
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II obtained by cassette ligation-mediated amplification of downstream
domain of coryneform bacterium sucrase gene, with sucrose-binding
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llarity 96.7%; Pred. No. 8.7e-314;
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Pred. No. 5.2e-29;
0; Mismatches 479; Indels 24;
                                                                                                                                                                                                                                                                                                            use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5840 BP; 1848 A; 944 C; 1256 G; 1779 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 389-392; 2084pp; English
                                                                                                                                                                                                                                                                           w isolated Enterococcus faecalis
used to develop products for the
                                                                                                                                                                                                  CA;
                                                                                                                                                                                                    Kunsch
                                                                                      97US-0066009.
97US-0044031.
97US-0046655.
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Best Local Similarity 48.3%;
Matches 470; Conservative (
                                                                                                                                                               SCI INC
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                                                                                                                                                                                                  Dillon PJ,
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                                                                                                                                                             (HUMA-) HUMAN
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06-MAY-1997;
16-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                       2490 aaactgataagatggtggcacctgtaaaaacgaatcaagaagacaaaattatttagcaa
                                                                                                                                                                                                                                                                                                                                 gcacgcactttaacccgctgaagaagcagggcgatgaagtcaaagcaggggagctgctgt
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                                                                    tcttac-----gttttgaagatcaacctaatccagaaacagcaactgaaaaaacag
                                                                                                                                                                            2550 gtccacttcaaggtgaaattttaccgctagaaaagtacaagaccctgtttttgcttcag
                                                                                                                                                                                                        2610 gtgctttaggaaaaggtgttgcaattgagccgactgaaggcaaactgtatgcacccgcag
                                                                                                                                                                                                                                                            737 giggaaagaitgiggiggcaitcccaictggccaigcittcgcagticgcaccaaggcig
                                                                                                                                                                                                                                                                                       2670 atggtgamatcaccacattatttccgacaggacatgctgttggcttgacgacaacagagg
                                                                                                                                                                                                                                                                                                                                                                                                  2778 gtaaaggctttgaattatcagtgaaacaaggtgattctgttaaaaaaggagatttgctag
                                                                                              560 ccaaagccgaagcagaagcacccgcagaattttcaaacgattccaccatcatccaggca-
                                                                                                                                                    --cetttgaccggtgaagctattgcactgagcagcgtcagcgatgccatgtttgccagcg
                                                                                                                                                                                                                                                                                                                  797 aggatggttccaatgtggatatcttgatgcacattggtttcgacacagtaaacctcaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidermidis genomic polynucleotide sequence SEQ ID NO:3464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 1030-1031; 2188pp; English
AAH54100 standard; DNA; 2913 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing only to SEQ ID NO:4455 to 4472, though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGCTTTAGCTGCATTCTTTATCATTAAGCAAAATAAAAAATTAAAAGGTGTTGCTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 2913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 120...
59.0%; Pred. No. 1.7e-27;
.ive 0; Mismatches 163; Indels
..ive 0; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2913 BP; 1072 A; 480 C; 419 G; 942 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            no sequences are present for SEQ ID NO:4455 to 4464.
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AAV52334/C
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524)

Tecorded on It, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO: 1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and sequence acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplification the number of the sequence of the molecules whose nucleotide sequence is homologous to amplification the number of the sequence of the sequence of the member of the sequence of the molecules whose nucleotide sequence is homologous to amplification the fragment of the S.pneumoniae genome to prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical compositions and vaccines for S. pneumoniae
                                                                                                                                                                                                                                                                                                                            Fannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3895 BP; 1166 A; 869 C; 805 G; 1055 T; 0 other;
                                                                                                                                                                                                                                                                                                                            Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1179-1182; 1409pp; English.
                                                                                                                                                                                                                                                                                                                         Dillon PJ,
                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                  97WO-US19588.
                                             Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                       Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-272225/24
                                                                                                                                                                                  30-0CT-1997;
                                                                                         WO9818931-A2
                                                                                                                                                                                                                                31-OCT-1996;
                                                                                                                                    07-MAY-1998
                                                                                                                                                                                                                                                                                                                         Barash SC,
Kunsch CA,
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2967 TCTTCGGTGCAATTTTTGGCGCCCTCTACGCTCCATTTGTCATCACAGGTCTGCACCATA 2908 2847 TGATTGCTCTTTCTAATATTGCTCAAGGCTCAGCCGTGTTTGCCTATTATTTCATGCATC 2788 GCCATGATGAGCGTGAGGCTTCACTTCCTGCAACCATTCCAGCCTATCTCGGTG 2728 136 cggcatctatggctaatatcgcccagggtgcggcatgtttggcagtgttcttcctggcga 196 Gaps 20 tcggcggtctgctcttcggtctggtctactcaccaatcgtcatcactggtctgcaccagt 79 80 ccttcccgccaattgagctggagctgttt---aaccagggtggatccttcatcttcgcaa 2907 TGACCAATGCCATTGATACACAATTGATTGCGGATGCTGGTGGCGCCTGTGGCCAA agagigaaaagcicaagggcc---tigcaggigcticaggigicticcgcigitictiggia 24; Length 3895; Pred. No. 4.5e-26; 0; Mismatches 477; Indels Score 118.8; DB 19; 10.78; Local Similarity 48.4 tes 469; Conservative Query Match Best Loca Matches 137 197 2787 δλ g ò g ò q ò q

254 ttacggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggta 313

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2667 IGACIGGIICAGCCCIIGCAGGCAIGIIAICCGIIACTIIIAAIGIAACIGCGGCIICIA 2608
                                                                                                                                                          2547 CAGGAACTATGCTTGCGATTGTTGTTCCAATGCTC-----TGACTTTCTTCTTCT 2494
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                                                                tgggcgctgcaggtttcttgggtgttgtttctattgatgctccagatatggtcatgttct 433
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Matches 490;
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Kunsch CA,
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                                                                                                                                                                               The nucleotide sequence of a 3615 bp probe obtained by digestion of secherical coll genomic DNA with the restriction enzyme HindIII.

The probes (AAQ55133-48 and AAQ55752-58) represent other probes derived, by HindIII digestion of the genomes of Staphylococcus aureus, Sepidermis, Enterococcus faecalis, Pseudomonas aeruginosa, E.coli, Klebsiella pneumoniae or Enterobacter Cloacae. The probes can be used to detect their respective microorganisms in clinical samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGTTGCGGGTCGAATTGCTTCGTTCGCCACATTACA-----CGCCATTGGCATT 1625
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                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                       Probe for identifying bacteria causing infectious disease -consists of a DNA fragment obtained by HindIII cleavage of the pathogenic bacterial genomic DNA
                                                                                                                                                                                                                                                                                                                      Length 3615;
                                                                                                                                                                                                                                                                                                                    8.2%; Score 91; DB 15; Length 36 llarity 53.7%; Pred. No. 1.7e-17; Conservative 0; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                 Sequence 3615 BP; 966 A; 962 C; 805 G; 882 T; 0 other;
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                                                            Uehara H;
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                                                                                                                                                         Claim 7; Page 62-64; 100pp; Japanese.
                                                            Ohno T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV52163 standard; DNA; 9769
92JP-0179719
                        PHARM IND LTD
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                                                            Matsuhisa A,
                                                                                 WPI; 1994-035086/04
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Best Local Similarity
Matches 240; Conserv
                       (FUSO ) FUSO
(OHNO/) OHNO
07-JUL-1992;
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52524) are genomic fragments from Streptcoccus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule sproding a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the collaboration sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating molecules whose nucleotide sequence is homologous to amplification or primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the computer based system for identifying readable meditum can be used in a computer-based system for identifying
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S. pneumoniae; genome; diagnosis; assay, vaccine; pharmaceutical composition; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumoniae genome of commercial importance,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9769 BP; 2918 A; 2141 C; 1792 G; 2916 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 90.2; DB 19;
46.7%; Pred. No. 5.1e-17;
tive 0; Mismatches 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon PJ, Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 318-324; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0029960.
                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US19588
    Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-272225/24.
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5;

EP786519-A2 30-JUL-1997

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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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               3543 TIGCIGGIGCAAICGCIGGIGGAIIGGCIICIAICCIIGGACIIGCIGGIACIGGIAAAIG 8484
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                                                                                                                                                                                                                                                                                                                                                                                                                     gaaagettggetcgggegttgecategteceaaceaaggggeagttagttteteeggtga 736
cggagcctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcg 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATCACCATCATCCTGGTACAATGCTTTATGTTGGTAACGGACAACTTCCACAATACC
                                                                                                                                                                                                                                        tggttcgccgcaacggcagcattgatccagatgcaaccgctgctccagtgcctgcaggaa
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                                                                                                                                                                                                                                                                                                                                                                                       8264 CTCCTATCGTCGTGATGTTGTCGCTCTTGCTGATGTCAATGACCCAGTCTTCTCAAGTG
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                                                           gtaccgcagctatcggtggcgctttgattgcactctttaatatcaaggcagttgcgttgg
                                                                                                                    gegetgeaggtttcttgggtgttgtttctattgatgctccagatatggtcatgttcttgg
                                                                                                                                                                               tgtgtgcagttgttaccttcttcatcgcattcggcgcagcgattgcttatggcctttact
                                                                                                                                                                                                                                                                    ACATGTTTGGTTACGAAG - - - ATGAAGTAGACGCAACTGCAGCTGCAAAACGAGCTGAAG
                                                                                                                                                                                                                                                                                                   cgaccaaagccgaagcagaagcaccgcagaatttcaaacgattccaccatcatccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtggaaagattgtggtggcattcccatctggccatgctttcgcagttcgcaccaaggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        797 aggatggttccaatgtggatatcttgatgcacattggtttcgacacagtaaacctcaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1976 GAACATTIGACTCAAACAAAATCGCTGCAGCTGGACTTGATGATACAACAATGGTTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus contig SEQ ID #1317.
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                           8603
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257
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Staphylococcus aureus.

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medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), raed-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection of polypeptides can also be used in a kit for the immunodetection of the sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used for recombinant same useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 ttaaaaactaagatatccatttattggcgctatcgttggatcaggtattggttcagcatat 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attgcactctttaatatcaaggcagttgcgttgggcgctgcaggtttcttgggtgttgtt 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 ggtgcggcatgtttggcagtgttcttcctggcgaagagtgaaaagctcaagggccttgca 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 tetgeegeagtatttteageattaettggtattaeagaaeeggetatgtttggtgtt-ae 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 attgctttcttcaaggttaaagcaatcgcattaggaactgctggattgccaggatttatt 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggtgcttcaggtgtctccgctgttcttggtattacggagcctgcgatcttcggtgtgaac
                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococous aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents one of 5191 Staphylococcus aureus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76.4; DB 18; Length 465;
Pred. No. 1.8e-13;
0; Mismatches 146; Indels 1:
                                                                                                                                                                                                         Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 465 BP; 155 A; 69 C; 88 G; 152 T; 1 other;
                                                                                                                                                                                                       Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1918; 3271pp; English.
                                                                                                                                                                                                       PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                       Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.98;
54.38;
                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                             96US-0009861.
                                                                                          97EP-0100117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                              WPI; 1997-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 175; Conserv
                                                                                                                             05-JAN-1996;
                                                                                          07-JAN-1997;
                                                                                                                                                                                                                         Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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1669 agcacaacaaaacactgttcacttcaaagatcttactgaggaagtttactcagtagcaga 1728

cggtgaagctattgcactgagcagcgtcagcgatgccatgtttgccagcggaaagcttgg

1789 tgatggatttgcagtagaacctgcaaatggaaacattgtatctccagtttcaggtactgt 1848

687

627

747 tgtggtggcattcccatctggccatgctttcgcagttcgcaccaaggctgaggatggttc

746

taacccgctgaagaagcagggcgatgaagtcaaagcagggggagctgctgtgtgaattcga

867 1957 927

tacagttcatgttgctgaaggacaaaaagttgcagcaggagatctccttgtcacagctga

caatgtggatatcttgatgcacattggtttcgacacagtaaacctcaacggcacgtt

gtcaagcatcttcccaacaaaacatgcttttggtattgtgacggaagcagg-----

1849

807

866

926

cttggatgctatccgtgcagcaggacgtgaaacttcaacagtagttgtcttcacaaatgg 2076

987 caagaaaaccggacctgtaaa 1007

Escherichia coli protein encoding nucleotide sequence SEQ ID NO:137.

(first entry)

21-SEP-2001

AAH81338;

BP.

AAH81338 standard; DNA; 1947

Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antiblotic; gene therapy; diagnosis; bacterial growth inhibition; ds.

Escherichia coli.

WO200148209-A2.

05-JUL-2001.

19-DEC-2000; 2000WO-US34419.

99US-0173005

23-DEC-1999;

tattgatgccattaaggctgcaggttatgaggtaaccacgccgattgttgtttcgaatta 986

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AAH81338
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                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptcoccus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the cucleic acid molecule sproduced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening citizenty which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating man, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification contains and isolating the amplified sequences. The computer computer of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer computer for indentifying readable medium can be used in a computer-based system for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and
                                                                                                                                                                                                                                                                                                                                                                                                   Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                S. pneumoniae; genome; diagnosis; ass
vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                   Fannon M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8494 BP; 2532 A; 1570 C; 1870 G; 2522 T; 0 other;
                                                                                     Streptococcus pneumoniae genome fragment SEQ ID NO:163.
                                                                                                                                                                                                                                                                                                                                   Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1052-1057; 1409pp; English.
                                                                                                                                                                                                                                                                                                                                 Dillon PJ,
AAV52296 standard; DNA; 8494 BP
                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                             97WO-US19588.
                                                                                                                                                                                                                                                                          960S-0029960
                                                         (first entry)
                                                                                                                Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                             Rosen CA;
                                                                                                                                                                                                                                                                                                                              Barash SC, Choi GH,
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-272225/24.
                                                                                                                                                                                     WO9818931-A2
                                                                                                                                                                                                                                           30-OCT-1997;
                                                                                                                                                                                                                                                                          31-OCT-1996;
                                                         23-OCT-1998
                                                                                                                                                                                                                07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pneumon lae
                            AAV52296;
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The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AHH81202 to AHH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation
                                                                                                                                                                                                                                                                                          nucleic acids encoding proteins required for Escherichia coli
                                                                                                                                                                                                                                                                                                                            proliferation, useful for screening for antimicrobial agents
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 180-183; 596pp; English.
                                                                                 Zyskind JW;
(ELIT-) ELITRA PHARM INC.
                                                                                 Forsyth RA, Ohlsen KL,
                                                                                                                                                              2001-457376/49
                                                                                                                                                         WPI; 2001-457376,
P-PSDB; AAG98282
                                                                                                                                                                                                                                                                                          Novel
```

ij

Gaps

12;

Length 8494;

Score 67; DB 19; Length 84 Pred. No. 7e-10; ); Mismatches 250; Indels

.; ;

Conservative

239;

Matches

6.0%;

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cgaagcagcagcagcagaattttcaaacgattccaccatcatccaggcacctttgac 626

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of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular microorganism species in proteins appearance. AMBR1295 to AAMB1489 encode the Escherichia coll proteins given in AAG98239 to AAB81481, and AAH81488 to AAB81491 cepresent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1508 cgccgattaccggtgatgtcgtggcactggatcaggttcctgacgaagcattcgccagca 1567
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                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 22; Length 1947;
Pred. No. 6.4e-10;
0; Mismatches 220; Indels 1:
                                                                                                                                                                                                                                                                                                             Sequence 1947 BP; 399 A; 498 C; 568 G; 482 T; 0 other;
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Similarity 48.7%;
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WO9850555-A2 12-NOV-1998

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982 nucleotide sequences isolated from the Enterococcus faecalis genome.
AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1751 AAAAAGTTAAAAGCTTTGTGTCCGCCAGCAATTATCTCTGGTATTTTTGGTGTAACAGAG 4692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 tctatggctaatatcgcccagggtgcggcatgtttggcagtgttcttcctggcgaagagt 201
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                                                                                                                                                                                                                                                                                                                                                                                                              computer readable medium has been developed which has recorded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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Pred. No. 2.7e-09;
0; Mismatches 238;
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                                                                                                                                                                                   Kunsch CA;
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                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                        97US-0066009.
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                 98WO-US08985
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                                                        14-NOV-1997;
06-MAY-1997;
                                                                                               16-MAY-1997;
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Matches 221;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoi H;
                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
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                                                                                                                                                                                                                                           C glutamicum coding sequence fragment SEQ ID NO: 3461.
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Senoh A, Ikeda M, Ozaki A;
                                                       AAH68426 standard; DNA; 2049 BP.
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03-AUG-2000; 2000JP-0280988.
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P-PSDB; AAG93207
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Tateishi N,
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                                                                                                                     AAH68426;
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Gaps

12;

Indels

Length 2049;

593 caaacgattccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcg

653

1523 caggigcaggagccgcigciggcgcigcaaccgccgiggcagciaagccgaagciggccg 1582

533 ccgctgctccagtgcctgcaggaacgaccaaagccgaagcagaagcaccgcagaattt 592

5.3%; Score 59.2; DB 22; 47.4%; Pred. No. 8.4e-08; iive 0; Mismatches 233;

Best Local Similarity 47.4 Matches 221; Conservative

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Query Match

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1763 cagiggcatigcgcittaga-----tagcggagitgaaatccitgiccacgitg 1810
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AX127152 Sequence AX122988 Sequence AX2711 Streptococc L32093 Pediococcus

AX127152 AX122988 STRSCRA PDCRAFOPER PPSURFOP APO01508

100.0 99.9 99.9 97.8 14.9 12.5 12.5 12.5 12.5

1107.4 1084.4 165.6 138.4 138.4 138.2 135.2 135.2 127.1 123.2 123.2

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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AX069136
Result
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                       nucleic search, using sw model
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232771 P. pentosace AP00150B Bacillus X69800 S. xylosus s X69800 S. xylosus s Z67015 Lactococcus AE004395 Vibrio ch AF26442 Staphyloc AX144742 Sequence AX144924 Streptoco M76768 Vibrio algi Z54245 B. subtilis AF07479 Streptoco B83967 Bacillus su 299108 Bacillus su Z99108 Bacillus su Z99108 Bacillus su AP001514 Bacillus su AF229829 Pseudomon M8177 Erwinia chr D37921 Alkalophiol AF206272 Streptoco X800503 B. subtilis AF206272 Streptoco M1038 E. coli; th M15746 E. coli; th M15746 E. coli; th M15746 E. coli bglC AR012068 Sequence AR025193 Sequence AR025193 Sequence

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ECOBGLO

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25-JAN-2001

PAT

AX069136 1109 bp DNA Sequence 3 from Patent WO0102583. AX069136

ALIGNMENTS

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AP001513 AE006630

292550 12086 136254 2134

BSTREPA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G. Orynebacterium glutamicum genes encoding phosphoenolpyruvat e: sugar phosphotransferase system proteins Patent: WO 0102583-A 3 11-JAN-2001; BASF AKTIENGESELLSCHAFT (DE) Location/Qualifiers 1. 1109

source

JOURNAL FEATURES

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.

(bases 1 to 1109)

Corynebacterium glutamicum. Corynebacterium glutamicum AX069136.1 GI:12579018

SUMMARIES

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Conservative
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Matches 1108; Conserv
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DEFINITION
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1 (bases 1 to 1527)
Pompeius,M., Kroeger,B., Schroeder,H., Zelder,O. and Haberhauer Orynebacterium glutamicum genes encoding phosphoenolpyruvat esugar phosphotransferase system proteins
Patent: WO 0102583-A 1 11-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
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Corynebacterium glutamicum
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Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
Iynuclectides
Ep 1108790-A 7068 20-JUN-2001;
KKO KOGYO CO., LTD. (JP)
Location/Qualifiers
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terium glutamicum
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2.1 GI:1464-
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Σ	g a	1618	TTAGTTTC
	Oy	781	
Corynebacterium. REFERENCE 1 (bases 1 to 1983)	q <sub>Q</sub>	1678	GTTCGCAC
	δλ	841	acagtaaa 
TITLE Novel polynucleotides JOURNAL Patent: EP 1108790-A 2904 20-JUN-2001;	ପ୍ର	1738	ACAGTAAA
KYOWA HAKH	Qy	901	gcagggga
source 1. 1983 /organism="Corynebacterium glutamicum"	අ <u>ධ</u>	1798	GCAGGGGA
/db_xref="taxon:1718" BASE COUNT 410 a 508 c 558 g 507 t	0y	961	
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/db_xref="GI:153801"
/translation="MDYSKVASEVITAVGKDNLVAAAHCATRLRLVLKDDSKVDQKAL
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MALIKLISDIFVPIIPPLAGGGLLMALNNFUTSEGLFGYTSLVQQFPIIKGSSDMIQ
IMSAAPEWELPILVGISAAKRFGANGFLGASIGMIWVAPGAANIIGLAAAPPSKAAT
IGAYTGFWNIFGLHVTQASYTYQVIPVLVAWULLSILEKFFHKRLPSAVDFTFTPLLS
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PAIETQLISAFQNGTGHGDFIFVTASMANVAQGAATFAIYFLTKDKKMKGLSSSSGVS
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KAQYUDEVLAAPLAGEAVEITSVNDPYFSSERAGKGIAIKPSGNIVVAPVDGTVOIAF
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                                                                                                                                                                                                                                                                                           J. Bacteriol. 171, 203-271 (2018) B9123027

B9123027

Draft entry and computer-readable sequence for [1] kindly provided by H.K. Karamitsu, 22-FEB-1989.

Location/Qualifiers
                                                                                                                                                                                                           1 (bases 1 to 2508)
Sato,Y., Poy,F., Jacobson,G.R. and Kuramitsu,H.K.
Characterization and sequence analysis of the scrA gene encoding
enzyme IIscr of the Streptococcus mutans phosphoenolpyruvate-
dependent sucrose phosphotransferase system
J. Bacteriol. 171, 263-271 (1989)
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                                               Streptococcus mutans sucrose-6-phosphate hydrolase (scrB) gene, partial cds; and enzyme scr-II gene, complete cds.
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                                                                                            M22711.1 GI:153799
enzyme scr-II; phosphoenolpyruvate-dependent sucrose
phosphotransferase system; sucrose-6-phosphate hydrolase.
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/note="sucrose-6-phosphate hydrolase (sciB)"
/codon_start=1</pre>
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/db_xref="G1:7272364"
/translation="MNLPQNIRY"
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/clone="pMH613"
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alpha-glucosidase; fructokinase; insertion element; permease; rafi
gene; rafR gene; raffinose operon; regulatory protein; scrA gene;
scrB gene; scrK gene; scrR gene; sucrase; sucrose-6-phosphate;
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IS30 homolog (transposable element Insertion sequence IS30 homolo
kingdom Prokaryotae) DNA; Pediococcus pentosaceus (strain PPE1.0)
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                                           tatcaaggcagttgcgttgggcgctgcaggtttcttgggtgttgtttctattgatgctcc
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The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
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TGRALDNRWSLYTLITUNLRIVELDPFGRAAIDRTKWSGHFFRWWVVGGTVSS
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KTATFARLGSTIGGGLVGVLVMPAVIFFSAKATSTGDNRGWFIFALIICLIALISAWG
VGGTRRUNDSDIRKNRODTVCVMEIRFARNDGLMAAATFFGYGTORIGGSLEVY
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IAGSNLMLVLLAAATMFGFPQQMVFLVVLMVITDSVEXGQLKLGHRDESLALSVRPLIF
TAGSNLMLVLLAAATMFGFPQQMVFLVVLMVITDSVEXGQLKLGHRDESLALSVRPLIF
DNA; Insertion sequence IS3 homolog (transposable element Insertion sequence IS3 homolog, kingdom Prokaryotae) DNA; and Pediococcus pentosaccus (strain PPEI.0) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="regulatory protein"
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| db_xref="GI:45107"
| /translation="MNGEYKTLANKSFESNVLFFGOEACLPNYTYKGNNVRDSYVIHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQEGKGTFAAANHPATVLKAGDIFILDKGTPCFYQADNDQPWKYFWIGFSAGIRIEAM
LSGSLLAQVCYLRQVQNGHYADLSELXVVJHTPNSLINDVLGSLITRRLFYDLLRWY
PADATNIKVKSTEGNLASYLQENYSTGTIMDLATLNLSRSYLYTLFRANTSP
QKLLTKLRLEDAKQRLSTSNNSVQSIANMVGYKDSFTFSKAFKRYSGASPSYYRKSIG
                                                                  Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                    On May 25, 1994 this sequence version replaced gi:475106.

Location/Qualifiers
1. 2183 Pediococcus pentosaceus"
/strain="PPEI.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'function="regulation raffinose-operon"
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/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="terminator 4"
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complement(2929. .3864)
                                                                                                                                                                                                                                                                                                                                     487, .510
/note="DR2; putative"
/rpt_type=direct
488, .561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3859. .3864)
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                                                                                                                                                                                                                                                                                                                                                                                                                          488. 561

/note="RRI; putative"

/rpt_type=inverted

513. 561

/note="DRI; putative"

/rpt_type=direct

2724. 2760
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3993. .5918
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3909.
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/gene="rafp"
                                                                                                                                 1 (bases 1 to 21838)
Leenhouts, K.J., Bolhum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="rafR"
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3909. .5918
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                                                                                                                   Pediococcus.
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                                                                                                                                                                                                                                                                         source
                                                                  ORGANISM
                                                                                                                                   REFERENCE
AUTHORS
TITLE
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CDS

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FGSLRGTSSHOWNPFLALVDHTTTEFSGDAYGFNLVYSGNHAFELEKDQLDQLHLMVG
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VNNWEATFPEPENEAKLKP IVDEAKQLG IEMFVLLDGWFGHRDDDNSSLGDWQVDHRKF
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DLGRQAVRNI FDQLDQLLKSKQIDY IKWDMNRHLSDIYSVALPPERQGEVYHRYVLG
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VQYKQI RPLIQFGGFFFLKSPTISNQAAMASGVLGYELDLTQLSSADKQIVQXOV
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LVGLNPKLNYQNIATRAIFGGDELMQLGFYDPVVXQDYTTKYYHFKAVTEN"
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TDVWBAACGBSMIGIAKDVPNSIYWTIGTGYGAGYISQNHIFNGRTHFELGHWRLNRL
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GLLLAQAALKNA"
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LRGTGFISYVEEGQHVQQGDELLEFWDPTIKQAGLDDTVIMTVTNSTEFTWMDMLVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGELRYPRVDRGFSGNLPGSTDRTFSRDTLPKBYSTAGEMDYHLPAAIVRHTDGANAL
YLVYQGYRIEAGKPKLSGLPAAFVEDETEAETLTIVLVDQVSQVEFDLQYTIYRDRPV
VTRSVQVCNQGDHAVNLEKVASMQIDFTDRQFETITLPGAHANERHPERGSINYGIQT
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/protein_id="AAA25564.1"
/db_xref="G1:475109"
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/protein_id="AAA25566.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="putative"
complement(10727. .11593)
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/gene="agas"
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/note="IR?; putative"
/rpt_type=inverted
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/rpt_type=direct
10396. 10442
/note="DR1; putative"
/rpt_type=direct
10397. 10443
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5976. .8177
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14519 CCGCATCAGCCATCGGATTCATTTCGATTGCTTCAAAGTCGATTCCAGCATTCATGCTCA 14460

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TETIVGPVLETVSDALTNGLVGLYNSTGWICKGIFGLLYSALVITGLHQTFFAIETQL
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TFIKAHFYRLPTTRHVVAWLIVTADKKQAICCYLNGLNSRVKTQHPLPLHYLDAELAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WNVFGLHVAQAGYQGQVLPVLGVAFILATLEKFFHKHIKGAFDFTFTPMFAIVITGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVNLNGEHFTTNVQKGDTVHQGDLLGTFDIAALKAANYDPTVMLIVTNTANYANVERL
TTLRHHGTTNLQVTALSSAQLDLPTDQYTALTLSGTHAHEANPSFNRLHPGLQTVRSL
                                                                                                                                                                                                                                                                                                        /function="enzyme II of the PTS system, sucrose specific"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14760
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                                                                                                                                                                                               SDSSGNRYTGHQLNTMGIPLKPTNADFTSQLIYLCQN"
complement(13852. 15989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.5%; Score 138.4; DB 1; Best Local Similarity 57.9%; Pred. No. 2.5e-27; Matches 272; Conservative 0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVTNVQAGEQLVALTAPAASSVAATTV"
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15993. 17568
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16017. 16022
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. (bases 1 to 21839)
Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G.
The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSGSLLAQKCYLRQVQNGHIYADLSELYKVLHIPNSLINDVLLGSLIYRLFYDLLRWY
PADATNIKVKSTEQFNLAVSYLQENYSTGCTIMDLCHYLNLSRSYLYTLFKTHANTSP
QKLLTKLRLEDAKQRLSTSNNSVQSIANMVGYKDSFTFSKAFKRYSGASPSYYRKSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation-"mnGgYrTLANKSFESNVLFFGQEACLPNYTYKGNNVRDSYVIHY
IQEGKGTFAAANHPATVLKAGDIFILPKGTPCFYQADNDQPWKYFWIGFSAGIRIEAM
                                                                                                                                                                                                       enzyme IIabc; fructokinase;
sucrase.
                                                                                                                                                                                                                                                                       Pediococcus pentosaceus
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-APR-1994) Leenhouts K. K., Institute for Biological Sciences, Department of Genetics, Kerklaan 30, Haren, The Netherlands, 9751 NN
                                                                                                                                     24-MAY-1994
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On May 26, 1994 this sequence version replaced gi:475962.
PPSURFOP 21839 bp DNA BCT 24.
P.pentosaceus (PPE1.0) sucrose and raffinose operons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pentosaceus"
                                                                                                                                                                                                               alpha-galactosidase; alpha-glucosidase; insertion element; permease; regulator;
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2929. .3864)
/gene="rafR"
complement(2929. .3762)
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/citation=[1]
complement(3859. .3864)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="PPE1.0"
/db_xref="taxon:1255"
487. .510
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/rpt_type=INVERTED
513. .561
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/rpt_type=DIRECT
488 .561
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Leenhouts, K. K.
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/note="IR1"
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                                                                                                                                                                                             GI:493728
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                                                                                                                                                                                                                                                                                                              Pediococcus.
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                     DEFINITION
                                                                                                                  PPSURFOP/c
                                                                                                                                                                                                                                                                          ORGANISM
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TITLE
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AUTHORS
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                                                                                                RESULT
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//processi_id="CAR83667.1"
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TDYNBAACGESMIGTAKDVPNSIYWTIGTGYGAGAYISQNHIFURGHTFLGHMKLNRL
PGDDFKSNCPYHDICLEGGLAAGPANGKRTGKAGKDIPVDDPVWPIITDYIAQACVNLT
                                                                                                                                                                                                                               QSLGRSIEQRPMMFNQRNRIGDFELDTVVGPRGHSKAVLLTLIDRKSRFLWAYRLKDR
TTATVNEALTKFLTTFNGPVHSFTVDRGTEFSGLVSLESQYGIKTYYCHAYTPADVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mnHQEVADRVLNAIGKNNIQAAAHCATRLKLVIKDESKIDQQAL
DDDADVKGTFFTNGQYQIIIGPGDVDKVYDALIVKTGLKEVTPDDIKAVAAAGQNKNP
                                                                                                                                                                                                          LNHLRLSWSPGMIAHEFKLATKSIYNWLNQGRIGFSLNDLPEHGVRQRRNVDQRSKYN
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WNVFGLHVAQAGYQGQVLPVLGVAFILATLEKFFHKHIKGAFDFTFTPMFAIVITGFL
                                                                                                                                                        /translation="SDAVRTKRSASLKWCLPQTHLLGADLLSSITYSERIKIETFCEL
                                                                                                                                                                             GLSNIQMGVRLNRSPSTISYELSRCQPYQAELAQTDAEYKRSQCGRKTKLSDELKQKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the PTS system, sucrose specific"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 ttgagctggagctgtttaaccag-----ggtggatccttcatcttcgcaacgg 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 21839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name="terminator 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name="fructokinase"
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                                                 /product="insertion element"
/protein_id="CAA83666.1"
/db_xref="GI:475966"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA83668.1"
/db_xref="G1:475968"
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                                                                                                                           /db_xref="SPTREMBL:Q52261"
                                                                                                                                                                                                                                                                           MNALIGIYVVFILKGLVLSTLVLKI"
10396. 10442
/note="DR1"
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/gene="scrA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_type=inverteD
10681. .10716
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complement(10727.
/gene="scrK"
                            /transl_table=11
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10397. .10443
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/citat
     /codon_start=1
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Matches 272;
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KFGGAISNGVVGQIAIISGMTGATASSTTAAGQLHFKLTMRAFPALMLLIAIGIFSR
GTETJEEKHAEIVAELERTWRTKFDNTDQVAEKVVTSLDLATPIAGQUPLAQVNDP
TFAAGTLGOGFAIRSDGRILAFPDATVRQVFTTRHAVGIVGDNGTVLLIHIGLGTVK
LRGTGFISYVEEGQHVQQGDELLEFWDPTIKQAGLDDTVIMTVTNSTEFTMMDWLVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGNKALDNRMVSLVTLIMVLRIVELFIDPFIGNAIDRTKNSPGHFRPWVVGGTVSS
IILLLFYNLGGLYAKNAMTYLWPRILYTTMDIFYSFRDVGFWSMLPSLTTDSRERE
KATFARLGSTIGGGLVGVLVMPAVIFFSAKATSTGDNRGWFIFALIICLIALISANG
VGLGTREVDSDIRKNSDTVGFWFIFALAKNDQLLWAALAYLFVGVGINILGSLEVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:P43466"
/translation="MQEEHNYKWVGGRLIYGFGAKGNDAFYSILSGYLIIFITSHLFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VTRSVQVCNQGDHAVNLEKVASMQIDFTDRQFETITLPGAHANERHPERGSINYGIQT
SCALRGTSRIGMNPFLALVHTTTERSGDAV GENLYYSGAHAPELEKODLDQLHEMVG
INSYNEWQLKAGAFTGYPEYLMYYTNKGINAMSQAYHHLIRERVVRSEFKNDERPIY
VNNWEATFFDFNEAKLKPIVDBAKQLGIEMFVLDDGWFGHRDDDNSSLGDWQVDHRKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYDISLATAHVSVSPNQQTGRETSMSTRSAVAASGVIGYELDLYQLSSADKQIVQKOV
VQYKQIRPLIQFGEFYRLKSPITSNQAAWMFVSPQQDEAIVMVFNLTSYAQPSLTKTK
LVGLNPKLNYQNIATKAIFGGDELMQLGFYDPVVYQDYTTKVYHFKAVTEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGELRYPRVDRGFSGNLPGSTDRTFSRDTLPREXSTAGEMDYHLPAAIVRHTDGANAL
YLVYQGYRIEAGKPKLSGLPAAFVEDETEAETLTIVLVDQVSQVEFDLQYTIYRDRPV
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/function="IS-30 (E.coli) like IS element"
                                                                                                                                                                                                                                                                                                     function="raffinose transport protein"
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/standard_name="terminator 3"
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/note="DR2"
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Takami, H., Nakasone, K., Hirama, C., Takaki, Y., Masui, N., Fuji, F.,
Nakamura, Y. and Inoue, A.
An improved physical and genetic map of the genome of alkaliphilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (sites)
Makami, L. and Horikoshi, K.
Reidentification of facultatively alkaliphilic Bacillus sp. C-125
to Bacillus halodurans
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14759 CCTCGATGGCCAACATTGGGCAAGGTGCCGCCACTTTAGCTATTTTCTTTGCTACTAAGA 14700
                                                                                                                             14519 CCGCATCAGCATCGATTCATTTCGATTGCTTCAAAGTCGATTCCAGCATTCATGCTCA 14460
                                                                                                                                                                                                                                                           260 agcctgcgatcttcggtgtgaaccttcgcctgcgctggccgttcttcatcggtatcggta 319
                                                                                                                                                                                                                                           ccgcagctatcggtggcgctttgattgcactctttaatatcaaggcagttgcgttgggcg 379
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Takami, H., Takaki, Y., Nakasone, K., Sakiyama, T., Maeno, G.,
Takami, H., Hirama, C., Fuji, F. and Masui, N.
Genetic analysis of the chromosome of alkaliphilic Bacillus
halodurans C-125
Extremophiles 3 (3), 227-233 (1999)
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Replication origin region of the chromosome of alkaliphilic
Bacillus halodurans C-125
                                              catctatggctaatatcgcccagggtgcggcatgtttggcagtgttcttcctggcgaaga
                                                                                                            200 gtgaaaagctcaagggccttgcaggtgcttcaggtgtctccgctgttcttggtattacgg
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Bacillus halodurans
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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Bacillus halodurans genomic DNA, section 2/14.
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AP001508.1 GI:10172890
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Extremophiles 3 (1), 21-28 (1999)
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TVDAQSTVWIWSRGITNVTDTRKTAYSNYYHRDSPHRSAAQLGNDRAVSPLGGPGATT
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Characterization and comparative study of the rrn operons of alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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                                                                                                                                                                        Takami, H., Nakasone, K., Ogasawara, N., Hirama, C., Nakamura, Y., Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K. Sequencing of three lambda clones from the genome of alkaliphilic
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Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
Horikoshi,K.
Genome analysis of facultatively alkalihilic Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                         Takami,H. and Horikoshi,K.
Analysis of the genome of an alkaliphilic Bacillus strain from industrial point of view
Extremophiles 4 (2), 99-108 (2000)
                                                     (in) Extremophiles in deep-sea environments (Ed.);
   HORIKOSHI, K. TSUJII;
   249-284; Springer-Verlag (1999)
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Extremophiles 3 (1), 29-34 (1999)
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Takami, H. and Takaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                         tecegecaattgagetggagetgtttaaccagggtggateetteatettegeaaeggeat 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             923 tcgatattgatgccattaaggctgcaggttatgaggtaaccacgccgattgttgtttcga 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagetateggtggegetttgattgeactetttaatateaaggeagttgegttgggegetg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aagccgaagcagaagcacccgcagaattttcaaacgattccaccatcatccaggcacctt
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                                                                                                                                                                                                                                                                                          Score 138.2; DB 1;
Pred. No. 3.5e-27;
0; Mismatches 493;
                                                                                                                                                                                                                                                                                        Query Match 12.5%;
Best Local Similarity 48.0%;
Matches 472; Conservative
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                                                                                                                                                                                                                                                                                                            TVA IY SMHGFSLFK TWRRLIGNACGVVFAVYLLFELDLAFALFGWOPRYLFAAMVTGS
DRELLLALSETEVPYSSRSSLIESTKNNYRTKELIVSOVAKVVALVSVTYFLLOIA
DRYFLLLALSETEVPYSSRSSLIESTKNNYRTKLEFILVSOVAKVVALVSVTYFLLOIA
NAAGALY IDAVLYEEBWARGKROYGEFY PHSTRVNPNYLQAFPLVDENNKR TA 10GEE
TNRVLLVPPROXKDOKED I AYFKEDYAYWATMPEVQAESY SHLQEOTFD I MLASSQE
YESHLLYYFPNEGNILVDP I LQVLFANNSY PMERPFRGSVGNDFLKYKLLDONTAKT
YEHYLPELRDLQLDDNAKHLYTYNNEGAQKD I SEIGRATLLOTILFYLTATIAFTYO
SSHLLFAQHKKRFLLRRLFGHSLFRAYRNULFWTLATTATIATIATIV
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                                                                                                                                                                                                                /translation="MHAWSAAAYADFAVTIPRIDLLGPDIVLSVLEEAATHHQVNLLR
VQLLGEGGGT ALTTFALLTEKSPFLEAIPLHHGSRLTSEDTRGDLIISSRRYEDV
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LEDYVBELEPLTADDFAVQTEPSHVSTTFDPTFPKTLAWTLWGITGLMMAFIHRNGK
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6023. .7096
7gene="BH0284"
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/db_xref="G1:10172897"
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                                                                                                                                            /transl_table=11
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/note="BH0282
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complement(4740. .5537)
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-DEC-1992) E. Wagner, Mikrobielle Genetik,
Universitaet Tuebingen, Auf der Morgenstelle 28, 7400 Tuebingen 1,
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complement(132. .137)
20737 ATGCAAAACAATTTTCAAATGTACAAACGACAGATAAGCGCGAGGTCACAAGTGAGGATT 20796
                                                                                                                                                                                                                10-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wagner, E., Gotz, F. and Bruckner, R. Cloning and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system
                                          983 attacaagaaaaccggacctgtaaacacttacggtttgggcgaaattgaagcgggagcca
                                                                                                                                                                                                                              S.xylosus scrA gene and unidentified open reading frames x69800
                                                                                                                                                                                                                                                                         membrane protein; scrA gene; sucrose transport protein Staphylococcus xylosus.
                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Staphylococcus xylosus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus xylosus
Mol. Gen. Genet. 241 (1-2), 33-41 (1993)
94049686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /isolate="cured strain C2a"/db_xref="taxon:1288"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<1. .121)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain-"DSM 20267"
                                                                                                                       20797 TGCTCATTCACGTCATAAAGTAA 20819
                                                                                                        1043 acctgctcaacgtcgcaaagaaa 1065
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                                                                                                                                                                                                                                                                                                     Staphylococcus xylosus
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1053. .2495
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1053. .2495
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/note="ORF2"
                                                                                                                                                                                                              2655 bp
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/gene="scrA'
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995. .1000
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-10_signal
RBS
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AUTHORS
TITLE
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SOURCE
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CDS
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                                                                                                                                                                                                                              İFANAPFTLLPILIGFSAAKREGGNAYLGAALGMILVHPELMSAYDYPKALEAGKEIP
HWILFGLEINOVGYQOLPMLVATIATIREKERKERKVIPTUDNLLFELLETGF
ITFSPYGPLRPILGYNLSDGLFWLYEFEGALGGLIFGLILYAPIVUNCHHISFIAIETO
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PAMFGYNULKLRYPFIGAIVGSGIGSATIAFFKVKAIALGTAGIPGFISISGONNGWLH
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Luesink, E.J., Marugg, J.D., Kuipers, O.P. and de Vos, W.M.
Characterization of the divergent sacBK and sacAR operons, involved
in sucrose utilization by Lactococcus lactis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2013 ATTACAGGTATGCATCATAGTTTTATTGCTATTGAAACGCAACTTATCGCTGACATTCA 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tatgatttcggcggtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2073 TCAACGGGTGGTTCATTTATATTCCCTATTGCAACAATGTCTAATATTGCACAAGGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcatgtttggcagtgttcttcctggcga---agagtgaaaagctcaagggccttgcaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 getteaggtgteteegetgttettggtattaeggageetgegatetteggtgtgaacett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 egectgegetggeegttetteateggtateggtacegeagetateggtggegetttgatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atcactggtctgcaccagtccttcccgccaattgagctgagctgtttaacca-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2133 GCTGCGCTTGCAGCGTTCTTTATTATAAAGAAAATAAAAATTAAAAAGCGTAGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 gcactctttaatatcaaggcagttgcgttggggcgctgcaggtttcttgggtgttgttct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 ----gggtggatccttcatcttcgcaacggcatctatggctaatatcgcccagggtgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sucrose gene cluster
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gene; sacR gene; sucrose-6-phosphate hydrolase.
Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 135.2; D
Pred. No. 1.7e-
0; Mismatches
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Bacteria, Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%;
60.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WDIFGFKVAQAGYQGQVLPVIGVAFILAKLERFFHKYLNDAIDFTFTPLLSVIITGFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALEGINLKLKYPFFIALGASAIGŠLFMGLFHVLAVSLGSAGLIGFISIKAGYNLQFM
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                                                                                                                                                                                                                                                                                                                                                                                             DNDPDLKGTFEAAGQYQIIVGPGDVNTVYBEFIKLTGISEASTADLKEIAGSQKKQNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3912 GGTGGAGACTTTATTTTCCAGTTGCGGCCTGCGCAAATATGGCTCAAGCTGGTGCAACT 3971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1092 TATCCGTTCTTTATTGCTCTTGGGGCTTCAGCAATTGGTTCATTATTATGGGATTATTC 4151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 133; DB 1; Length 58
Pred. No. 7.3e-26;
); Mismatches 415; Indels
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4848. 5720
                                 /gene="sacB"
2837. 2847
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49.3%;
                                                                                                                                     2872. .2877
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                                                                     2837. .2843
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                                                                                                                                                                                                            /qene="sacB"
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/qene="sack
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Matches 429; Conserv
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                                                                     -10_signal
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                                                                                                                                       RBS
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QTTDHFRDPQIFSEGGGIYCLIGAGSSOGNGIIKLYKAIENNILTDWRCDLGNLDFSKER
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GOLNIDDGFFDCYATOSFNAPDGSSAYAISMLGLDFTSYPTDKYNVGGYLSWYKKLSIK
DNKLYQYPVEKMKELRQMEQDLLLADNNIITSNSYELEVDFRQQTSTLLSLATNEKGD
SALKVEEDKENNFILLRNYEKRLAHVKIEKMNVFIDQSIFEIFINDGEKVLSDCRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIPNAAARSLQGKSLKLIGLVFPTIKNIFYAELIEKIEQALFIRGYKAMLATTEÄDEQ
KERDYLALLLSNQVDGIIYGSHNLKAHDYIAIEAPIVAFDRLLTPETTVVSSDNFEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILATKALINSGSKKTAIFTGNDNTNSPTYLRRDGYLLELERNQLKPHIIKIPSGWTLL
RKKVEIKKILENNDFDGVFCTDDLTAILVKDLASNLKKSLNVVGFDGTEFIENYYPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MIKLEDVANKAGVSVTTVSRVINRKGYLSDATISKVEKAMQDLH
                                                                              Direct Submission
Submitted (24-JUN-1997) Luesink E.J., Department of Biophysical
Chemistry, Netherlands Institute for Dairy Research (NIZO), P.O.
BOX 20, Ede 6714 BA, THE NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTIKQPINDLAELLVDLIIRKIDGDNIDITYQLPVQLHYGID"
complement(join(1283. .2704,2721. .2725,2737. .2743,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="sucrose-6-phosphate hydrolase"
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/db_xref="GI:4581476"
Bacteriol. 181 (6), 1924-1926 (1999)
                                                                                                                                                                                                                               lactis"
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/gene="sacA"
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/gene="sacR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1390, 1396)
/gene="sacR"
complement(1390, 1396)
                                                                                                                                                                                                          1. .5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1294. .1298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1416. .1422)
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                                                                                                                                                                                                                                                                                                  complement(330. .1286)
                                                                                                                                                                                                                                                                                                                                        complement(330, .1286)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="sacA"
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                                        2 (bases 1 to 5800)
Luesink, E.J.
J. Bacter
99173919
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                                                                          1. .10264
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                                                                                                                                                                                                         /note="biotype: El Tor"
complement(114. .1553)
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                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C. and White, O.

DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
1 (bases 1 to 10264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE004395 10264 bp DNA BCT 31-JUL-2000 Vibrio cholerae chromosome II, section 52 of 93 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTGACCCTGTTTTCTCAAAAGAAATTATGGGAAAAGGTATTGCAATCAAGCCTAAATCT 4496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4332 AATGC-----AACAACTCAATACCAACTGAGAAAGTTATTATGGATCCA 4376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4557 TATGGTATAAAAACAAAAATGGAGGT------GAAGTTCTTTACATATTGGA 4604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4665 GTAAAAGCAGGGGATTTACTAGGATCTTTTGATAAAGAAGAAATCAAGAAGAGGGGGATTG 4724
                                                                                                                                                            714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ttcgcagttcgcaccaaggctgaggatggttccaatgtggatatcttgatgcacattggt 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4605 ATAGATACTGTTTCAATGAATGGTAATGGATTCATACAAAATGTTAAAGTTGGCCAGAAA 4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttcgacacagtaaacctcaacggcacgcactttaacccgctgaagaagcagggcgatgaa 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gicaaagcagggagcigcigitgigaaiicgaiatigaigccaiiaaggcigcaggiiai 954
                   ccagatatggtcatgttcttggtgtgtgtgtgttaccttcttcatcgcattcggcgca 474
                                                                                                                  gegattgettatggeetttaettggttegeegeaaeggeageattgateeagatgeaaee
                                                                                                                                                                                                           gotgotcoagtgootgoaggaacgaccaaagccgaagcagaagcacccgcagaattttca
                                                                                                                                                                                                                                                                                                       aacgattccaccatcatccaggcacctttgaccggtgaagctattgcactgagcagcgtc
                                                                                                                                                                                                                                                                                                                                                                                                     gggcagttagtttctccggtgagtggaaagattgtggtggcattcccatctggccatgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4725 GATGATACTGTAATTATTGTTACAAATT 4755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaggtaaccacgccgattgttgtttcgaatt 985
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AE004395.1 GI:9658068
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Vibrio cholerae
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Gaps

12;

417

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 gatgetecagatatggteatgttettggtgtgtgeagttgttacettetteategeatte 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 AATCCACAGCAAATTGGTTACTACATCATGGGTATGGCGATCTCATTGTGGCCGCCTTT 177
                                                                                                                                                                                                                                                                                                                                                                                   656 TATGACTCGGCAGGGTTTGTCGGTGCCGCACTGTTTGGCTTTATCTATGCTCTTTTGTG 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 ITAITCAATGTAAAAGCCCAAGCGCTAGGCGCGGGCTGGTTTGCCAGGGATCATTTCGATT 237
                                                                                                                                                                                                                                                                                                                                          1 tatgatttcggcggtccagtcggcggtctgctcttcggtctggtctactcaccaatcgtc 60
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Pasteurella multocida PM70 section 189 of 204 of the complete
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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                                                                                                                                                                                                                                                                                                                                                                                                                               61 atcactggtctgcaccagtccttcccgccaattgagctggagctgtttaacca-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 ACCACGGGTGGCACCTTTATTTTCCCTATCGCTGCGATGTCTAACATTGCGCAGGGCGCC
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May,B.J., Zhang,Q., Li,L.L., Paustian,M.L., Whittam,T.S.
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                                                                                                                                                                                                                                                  Length 10264;
                                                                                                                                                                                                                                                  Score 127; DB 1; Length 10
Pred. No. 3.5e-24;
); Mismatches 200; Indels
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Zhang,Q. and Kapur,V.
Direct Submission
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Best Local Similarity
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WORKEVGGYVSPDPNLREEWASEDQELGATVMRAVGLADVVKFSEEELQFLTGTOSIEE
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6008. 7546
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complement(9444. .10067)
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complement(7648. .9258)
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                                 complement(4859. .6283)
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PHWHGANROVIPIALBRWRKTPFTALTRROWKTYRTLLQSEGYDAVIDAQGLLKSALF
ATRARGTRHCYDRHSITEPTAACTRYKYAISYQQHAVERIRQLFAQSLUYPLPHTQ
GDYGIARHFPOHAQTYRYVLFFHGTTRQDKFLPBTGORGHTLARKLTAGGIQIHVPWSNS
QERQRAERIAQGLDLVTILPKSTLSELAQQIVNASAVVSVDTGLAHLSAALDKTNLTL
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LRRGWKGESRYLJENDLRSNKKDYPMWYQRYIALAFEKGAVPKAEDLERRYPYITVDP
YQQHTLKKFEKQTALISPRSY
FGSAKDERAGEEIRGALFETMRHFCINLAGGFSLNEAYDLIAACTAIVTNDSGEMHIA
AAVQRPLVALYGPTSPTYTPPLSEKAVIIRLIEGGLIKVRKGKDSDEGYHQSLIDIQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MVNCRIGSLEILHKQLGHQSIVNCRIGSLEKDSRAGRKSYSVNC RIGSLESLCIAFFNSTYVNCRIGSLEKNQNLHLFHLDVNCRIGSLERIY"
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/db_xref="GI:12722271"
/translation="MKSLTQLLFILTALLPTSLFAHIHVEQAQMFSAKAGEPSAIFMN
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Submitted (24-OCT-2000) Department of Veterinary Pathobiology, University of Minnesota, 1971 Commonwealth Ave., St. Paul, MN
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/db_xref="GI:12722267"
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/protein_id="AAK03927.1"
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/db_xref="G1:12722270"
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/gene="PM1841"
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/gene="PM1842"
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480 c 419 g 942 t
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                                                                                                                              Score 123.2; DB 1;
Pred. No. 3.7e-23;
0; Mismatches 163;
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/db_xref="taxon:32630"
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/strain="SR1"
/db_xref="taxon:1282"
/clone="step.1003e09"
a 480 c 419 g 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 2913)
Kimmerly, W.J., Taylor, J. David, Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Ashanti, C., Allshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D. H., Miller, G.S. and
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2 (bases 1 to 2913)

1 Taylor, J.David, Kimmerly,W.J., Nelsen,A.J., Godlevski,M.M.,
Raylor,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
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Staphylococcus epidermidis strain SR1 clone step.1003e09 genomic
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                                                                                                                                                                                                                       aaccagggtggatcettcatettcgcaacggcatetatggetaatatcgcccagggtgcg
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                                       Length 10085;
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Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                     DB 1;
                                     Score 126.6; DB 1,
Pred. No. 4.6e-24;
0; Mismatches 199,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:9664743
                                       11.4%;
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                                                                       Conservative
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/traislation-"MKKNFKIRISTLLIVILVYFAVLLIVNETKLFKNDVNYSFDEA
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PAQHQXASDIKWADKIAKLMAKSYKQFGIKKDDIRQTYYK"
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complement (4247 . . 7201)
                                                                                                                                                                                                                                                                                                                                                                     TEGFKWMKSTYVLINASRGPIVHEQALVQALKDNEIEGAALDVYEFEPDITDDLKSLN
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complement(1080. .2204)
complement(1080. .2204)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSKVLYQGYTCFRGLIDDIDLKHPDCAKEYWGRKGRVGIVPLLNNQAYWFITINSKEN
NHKYSSFGRPHLQAYFNHYPNEVREILDKQSFTGILLHNIYDLKPLKSFVYGRTILLG
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GKIAOYRSRLEYAYNRIMKMMPNALAAGQTKFLYKSKEK"
COMPIEMENT (2515. .3291)
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                                                                                                         to glycerate dehydrogenase"
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/note="similar to autolysin
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35. .988
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/gene="SAV2305"
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Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori,M.,
Misumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Ui,Y., Kobayashi,N., Tanaka,T., Sawano,T., Inoue,R.,
Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S.,
Yoshino,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus subsp. aureus Mu50 (sub_species:aureus Mu50,
2034 GCGCGGGTATTTCAGCTTTACTAGGAATTACAGAACCAGCAATGTTTGGTGTCAATCTT 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete sequence, section 8/9.
AP003355 BA00017
AP003355.2 GI:14248078
                                                                                                                                                                                                                                                                                                                                                                                                         285
                                                                                                                                                                                                                                                                                                gcatgtttggcagtgttct---tcctggcgaagagtgaaagctcaagggccttgcaggt 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 cgcctgcgctggccgttcttcatcggtatcggtaccgcagctatcggtggcgctttgatt 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 gcactctttaatatcaaggcagttgcgttgggcgctgcaggtttcttgggtgtttttt 405
                                                                                   atcactggtctgcaccagtccttcccgccaattgagctg------gagctgttt 108
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Staphylococcus aureus subsp. aureus Mu50
Bacteria; Firmicutes; Bacillus/Clostridium group;
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COMPIEMENT (8884. .9681)
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LINSDVDQYTDTPSYKRTSCRLEVITKRGKSPLNPNNFRVNKKRHPQYSVQVQKKWER
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YETTEVATOTEVAHOOYSETAMELELMKMFEVPAFLLYUVGYYETYEI
FRHILIGELGKKFNFIAMSIVSVFLFAFIHVTDAKSPPEFGPYLLILSIILVFTYLKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to lyt divergon expression attenuator LytR"
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/gene="SAV2310"
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complement(8884. .9681)
/gene="SAV2311"
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Search completed: March 22, 2002, 08:55:40 Job time: 8049 sec

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/transl_table=11
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/product="hypothetical protein" /
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Pred. No. 2.1e-22;
RNLGSTIALHIANNFVSFVISVISIYA"
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              11569. .11898
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11569. .11898
                                                           /gene="SAV2314"
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                                                                               /codon_start=1
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ilarity 55.9%;
Conservative
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Matches
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Q9cgg4 lactococcus
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Q99x32 staphylococ
Q9bx92 staphylococ
Q9bx93 staphylococ
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Q57071 staphylococ
Q9cmq pasteurella
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 250E26F7664D4204 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENZYME II SUCROSE PROTEIN (EC 2.7.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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Interpro; IPR001996; PTS_BIIB.
Interpro; IPR001996; PTS_BIIB.
Interpro; IPR00396; PTS_BIIC.
Pfam; PP00358; PTS_BIIA.1; 1.
Pfam; PP00378; PTS_BIIA.1; 1.
Propom; PD002243; PTS_BIIC; 1.
PROSITE; PS00371; PTS_BIIA,1 1.
PROSITE; PS01035; PTS_BIIA.1; 1.
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 650 AA;
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SEQUENCE FROM N.A.
 NCBI_TaxID=1358;
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SEQUENCE 6
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                                                                                                       March 21, 2002, 16:28:26 ; Search time 43.43 Seconds
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Q91461 l
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Q95g6 c
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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    protein search, using sw model

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Maximum Match 100%
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EMBL; APO01508; BAB04015.1; -...

InterPro; IPR001127; PTS_EIIB.

InterPro; IPR001996; PTS_EIIB.

InterPro; IPR00358; PTS_EIIA.

Pfam; PF00358; PTS_EIIA.1; -...

Pfam; PF00378; PTS_EIIA.1; -...

Pfam; PF00378; PTS_EIIE.1.
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                                   175 PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQ------APLTGEAIALSSVSDAMFASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IALFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID
                                                                                                                                                                                                                                                                                                                                                                            227 KLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT.
BH0296.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Me Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630 AA; 66978 MW; 6F0218011686ADD5 CRC64;
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NCBL_TaxID=86665;
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PROSITE; PS00371; PTS_EITA_1; 1.
PROSITE; PS01035; PTS_EITB_CYS; 1.
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Horikoshi K.;
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01-OCT-2000
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120 IKAVALGAAGFLGVVSI---DAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD 176
                                                      SVAVAPGAPGLLTIPIFYPEDGRGFVAFVIAIIISFVLA----AVLTYIVGFKDPVDDE 456
                                                                                                  177 ATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP 236
                                                                                                                   237 TKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQG 296
                                                                                                                                                                                      60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).

EMBL, APOOLSO9; BAB043441...

InterPro; IPR001127; PTS_EIIA.

InterPro; IPR003352; PTS_EIIB.

InterPro; IPR003352; PTS_EIIB.

PF00358; PTS_EIIA_1: 1.
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                                                                                                                                                                                                                                                     297 DEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
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STRAING-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
HOTIKOSHI K.;
                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDE-SPECIFIC ENZYME II, ABC COMPONENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=86665;
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01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
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Pfam; PF02378; PTS_EIIC; 1.
Probom; PD001476; PTS_EIIB; 1.
PROSITE; PS003243; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIA_1; 1.
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Matches 132; Conserv
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Best Local Similarity
Matches 118; Conserv
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MEDLINE-21192684; PubMed=11296296;
MEDLINE-21192684; PubMed=11296296;
MEDLINE-21192684; PubMed=11296296;
MEDLINE-21192684; PubMed=11296296;
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Olan Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
Tomplete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
COMPLETE PROTECOME.
                                                                                                                                                                                                                         : ||:| ||:| :: | ||: | : | 555 LLQPTEGVLVAPCDAEVSVLFPTKHAICLVTT----EGLELLMHIGMDTVNLDGGGFEAL 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LAVFFLAKSEKLKG-LAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIAL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 FNIKAVALGAAGFLGVVSIDAPDMVMFLVC----AVVTFFIAFGAAIAYGLYLVRRNGSI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 AIVPIKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPL 292
                                                                                                                                                                                                  QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PTS SYSTEM ENZYME II.
SPY2097
Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
175 PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAI
                                 235 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK
                                                                                                                               |::|:| ||||| : :|: || : |
|S21 EPSEGKLFSPVSGMVTALYPTHHALGITT----DRGAELLIHIGLDTVQLDGKFFTAHTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.6%; Score 539.5; DB 2; Length 36.6%; Pred. No. 2.5e-25; ive 67; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        674 AA; 72490 MW; 4BAA26B40E784878 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus.
NCBI_TaxID=1314;
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099XQ4;
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ID Q9L8G6
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58 CLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIAL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 NKETVNKDIKVEEVES------VVSPVNGKVVLLKNVPDKTFAEGLIGDGIGVDPE 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD 297
                                                                                                                                                                                                                                                                                                                                                                                                 sucrose transport and metabolism
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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PROSITE; PS00371; PTS_EIIA_1; UNKNOWN_1.
PROSITE; PS00134; TRYPSIA_HIS; UNKNOWN_1.
SEQUENCE 627 AA; 67596 MW; B835AB0238FCA436 CRC64;
                          Last sequence update)
Last annotation update)
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Last annotation update)
PERMEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNT 337
                                                                                                                                                                                                                                                                                                                                                             Tangenery M., Mitchell W.J.;
Tangenery M., Mitchell W.J.;
"Analysis of a catabolic operon for sucrose train Clostridium acetobutylicum ArCC 824.";
J. Mol. Microbiol. Biotechnol. 2:71-80(2000).
EMBL, AF205034; AAF35839.1;
InterPro; IPR001127; PTS_EIIB.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR001354; TTYPsin.
Pfam; PF00358; PTS_EIIA.1;
Pfam; PF00357; PTS_EIIA.1;
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MEDLINE=20391269; PubMed=10937490;
01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
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EMBL; AE006608; AAK34540.1;
                         620 AA;
              Complete proteome. SEQUENCE 620 AA;
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                                                          Cote C.K., Cvitkovitch D., Beliacis A.S., Honeyman A.L.;

"A novel beta-glucoside-specific PTS locus from Streptococcus mutans
that is not inhibited by glucose.";

Microbiology 146:1555-1563(200).

"BEBL; AF206272; AAF89975.1; -
"R InterPro; IPR001127; PTS_EIIA."

"R InterPro; IPR001396; PTS_EIIA."

"R InterPro; IPR003352; PTS_EIIA."

"R InterPro; IPR003352; PTS_EIIA."

"R Pfam; PF00358; PTS_EIIA...

"R Pfam; PF00378; PTS_EIIA...

"R Pfam; PF00378; PTS_EIIA...

"R Pfam; PF00378; PTS_EIIA...

"R ProDom; PD002243; PTS_EIIA; 1.

"R ProDom; PD002243; PTS_EIIA; 1.

"R ProDom; PD002243; PTS_EIIA; 1.

"R PROSITE; PS00371; PTS_EIIA, 1.
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                                                                                                                                                                                                                                                                                                                                                                                             60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                120 IKAVALGAAGFLGVVSIDAPD----MVMFLVCAVVTFFIAFGAAIAYGL-YLVRRNGSID 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 PDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                          1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIE-LELFNQGGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                        28.4%; Score 517; DB 2; Length 644; 35.0%; Pred. No. 5.5e-24;
                                                                                                                                                                                                                                                                                                  65; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SUCROSE-SPECIFIC PTS PERMEASE, ENZYME II.
SCRA OR SPY1815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 AA.
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                                                   MEDLINE=20340959; PubMed=10878120;
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MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                     Best Local Similarity
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SEQUENCE FROM N.A.
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                 Matches 126;
                                       STRAIN-NG8;
                                                                                                                                                                                                                                                                          Query Match
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and
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                                                                                                                                                                                                                                                                                                      62 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                                                                                                      20; Gaps
                                                                                                                                                                                         3 FGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAACLAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown G.D., Thomson J.A.; "Isolation and characterisation of an aryl-beta-D-glucoside uptake elibration system (abg) from the gram-positive ruminal Clostridium species C. longisporum." Mol. Gen. Genet. 257:213-218(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 VSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 VPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium longisporum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-B6405;
A Brown G.D., Thomson J.A.;
Brown G.D., Thomson J.A.;
Brown G.D., Thomson J.A.;
Cubilities (DEC-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L49336; AGC05713.1;
R HSSP; P20166; 1GPR.
R InterPro; 1PR001127; PTS_EIIA.
R InterPro; 1PR001352; PTS_EIIA.
R InterPro; 1PR003352; PTS_EIIA.
R Pfam; PF00358; PTS_EIIB.
R Pfam; PF00358; PTS_EIIB; 1.
R Pfam; PF00378; PTS_EIIB; 1.
R Pfam; PF00378; PTS_EIIB; 1.
R Probom; PD001476; PTS_EIIB; 1.
R Probom; PD001475; PTS_EIIB; 1.
R Probom; PD001243; PTS_EIIB, 1.
R PROSTITE; PS00321; PTS_EIIA_1; UNKNOWN_1.
                                                                                Length 620;
                                                                                                                                   Indels
  64F5FE83524DC4DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 GELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                             27.1%; Score 494; DB 2; L 36.8%; Pred. No. 1.4e-22; ive 47; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98151780; PubMed-9491080;
65725 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-UDIV-2001 (TrEMBLrel. 17, PTS-DEPENDENT ENZYME II.
                                                                                Query Match 27.1%
Best Local Similarity 36.8%
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Query Match

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290 LAGAAMGALWQVCVIFGLHWGLIPLMINNLAVLGHDSMMPMLLPAVMGQVGAALGIFLRT 349
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                    LAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALF 118
                                                                                                                                              ----FLG-----VVSIDAPDMVMFLVCAVVTFFIAF 156
                                                                                                                                                                                                                      157 GAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFS-----NDSTIIQAPLTGE 211
                                                                                                                                                                                                                                                                                          212 AIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNV 271
                                                                                                                                                                                                                                                                                                               phosphotransferase genes: functional expression in recombinant Escherichia coll and identification of a putative binding region for disaccharides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACLAVFFLA 65
 1 YDFGGPVG-GLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                DF1DE2A2A7B81339 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-97176370; PubMed-9023916;
Lai X., Davis F.C., Hespell R.B., Ingram L.O.;
"Cloning of cellobiose phosphoenolpyruvate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
CELLOBLOSE-SPECIFIC PTS PERMEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.7%; Score 468; DB 2; Best Local Similarity 33.0%; Pred. No. 5.3e-21; Matches 120; Conservative 67; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl. Environ. Microbiol. 63:355-363(1997).
EMBL; U61727; AAB51563.1; -.
HSSP; P20166; 1GPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO01127; PTS_EIIA.
InterPro; IPRO01996; PTS_EIIB.
InterPro; IPRO01996; PTS_EIIB.
InterPro; IPRO0352; PTS_EIIB.
Pfam; PPO0367; PTS_EIIB.; 1.
Pfam; PPO0378; PTS_EIIB.; 1.
ProDom; PD001476; PTS_EIIB.; 1.
PRODOM; PD002243; PTS_EIIB.; 1.
PROSITE; PS00371; PTS_EIIA.; 1.
PROSITE; PS00371; PTS_EIIA.; 1.
SEQUENCE 621 AA; 65492 MW; DF1
                                                                                                                                              119 NIKAVALGAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella oxytoca
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Q48408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                        120 IKAVALGAAGFLGVVSIDAPD------MVMFLVCAVVTFFIAFGAAIAYGLYLVRRNG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSG 231
                                                                                                                                                                                                                                                                                                                                                                                 450 EEEVKTTESKKEESLVKQEE-----IVSPIQGEVVTLAEVKDEAFSSGALGKG 497
                                                                                                                                                                                                                                                                                                                                                                                                                       VAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLN 351
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                                                                                            Gaps
                                                                                                                           1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus plantarum.
Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marasco R., Salatiello I., De Felice M., Sacco M.;
A physical and functional analysis of the newly identified bylgproperation of Lactobacillus plantarum.";
FEMS Microbiol. Lett. 186.269-273(2000).
InterPro: IPR001127: PTS_EIIA.
InterPro: IPR001956: PTS_EIIA.
InterPro: IPR001352; PTS_EIIA.
                                                                                       33;
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                                                     Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 577;
                                                 26.4%; Score 480.5; DB 2; Length 31.9%; Pred. No. 9e-22; ive 62; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88; Indels
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Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF00278; PTS_EIIB; 1.
Propom; P002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA, 1.
SEQUENCE 577 AA; 60877 MW; E8C877050103B5FC CRC64;
7D9CD1B17BE9283E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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STRAIN-B21;
MEDLINE-20263773; PubMed-10802183;
65890 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 17, I
                                                                    Best Local Similarity 31.9%;
Matches 115; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.3
Best Local Similarity 34.1
Matches 118; Conservative
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AA;
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919
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01-OCT-2000 (
01-JUN-2001 (
PERMEASE.
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SEQUENCE
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09L461 09L461;

RESULT **09L461** 

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48;

Length 621; 129; Indels

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408 AYTMGA---LGIFSFTSNITLTGEVSGAIKIMIVSAVAVIAGFVVTYLV----GFEDDVI 460
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Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus.
NCBI_TaxID=1314;
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                                                                                                                                                                                                                                 231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
350 RDARQKVLAGSAVSAGIFGVTEPAIYGLNLPLRRPFIFGCVYWPIGGAMVG-FSDSHVST 408
                                                                                                                                                               291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                     122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGL---YLVRRNGSIDPDAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                            126 GAAGFLGVVS-----IDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD
                                                                                                                                                                                                                                                            |||||:|| ||:::|| ||::|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 FNPIIFGLVLGFAWQVLVMFGLHWAIVPFAIIALAKGEPTALLIAASVASFAQTGAVGAV
                                                                                                                                    177 ATAAPVPAGTTKAEAE-----APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGCKG;
QGCKG;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE-SPECIFIC PTS SYSTEM IIABC COMPONENT (EC 2.7.1.69).
                                                                                   ----VWGGAAGMFASLII-----
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InterPro; IPR001349; ABC_transportr.
InterPro; IPR001197; PTS_EIIA.
InterPro; IPR001196; PTS_EIIB.
InterPro; IPR001352; PTS_EIIB.
InterPro; IPR001351; PTS_EIIB.
Pfam; PF00358; PTS_EIIA.; 1.
Pfam; PF00378; PTS_EIIA; 1.
ProDom; PD001476; PTS_EIIB; 1.
ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 448; DB 2;
Pred. No. 9.2e-20;
                                                                                 409 YSFGFGNIITLAQMIPPEGIDAT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67630 MW;
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33.0%;
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Best Local Similarity 33.0
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 0:0-0(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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618 SVSR 621
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Q9CFK9
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Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.S., D. Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an Ml strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                         70 LKGLAGASGVSAVL-GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIIGLPQYINPSGGANFTNALIAGTATIVLAFSLTWFMG-----IDEE---SPKQV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATASMA-NIAQGAACLAVFFLAKSEK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 ILGAIMPLVVMTGMHWAFAPIFLAASVATPDVLILPAMLASNLAQGAASLAVAFKTKQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| |:||:|| || || || || || || || || || 348 TRQVALAAGISALLAGITEPALYGVTLKFKKPLYAAMISGGLVGAFIGFVNIASYTFVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 GFLGVVSIDAP----DMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVAADMSQVKSGLSTKQT-LYAPMTGEMLFLSEVPDETFSSKLLGEGFAILPSEGEVYAP
179 AAPVPAGTTKAEAEAPAEFSNDST---IIQAPLTGEAIALSSVSDAMFASGKLGSGVAIV
                                                                  461 ENPIP------DKKFNKQKTNKEIIGSPLEGKVIPLSQVKDAAFSAGVMGKGAAIE
                                                                                                                                        PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66148 MW; 1AF6872CFDD7C7D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE PERMEASE IIABC COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%; Score 445.5; DB 2; 33.0%; Pred. No. 1.3e-19; ive 63; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                    GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
                                                                                                                                                                                                                                                                                                                     620
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STRAIN-SF370;
MEDLINE-21192684; PubMed-11296296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | : ||| | : || : :|||;|
| LLKMDIDFITSKGYSLISPVVVTN 594
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Query Match
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Q9KLT8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 ----GVPAQEEDQETINHIIAEKGKDKNLRTSSLGNVVEGEVISLNEVKDQAFSTGALGK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 IKAVALGAAGFLGVVS-IDAPDMV--MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAPVPAGTTKAEA--EAPAEFSNDSTIIQAPL----TGEAIALSSVSDAMFASGKLGS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 VGGLLFGLVYSP----IVITGLHQSFPPIELELFNQGG---SFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                        Franz C.M.A.P., Wordbor R.W., Quadri L.E.N., Schillinger U.,
Holzapfel W.H., Vederas J.C., Stiles M.E.;
"Atypical genetic locus associated with constitutive production of
enterocin B by enterococcus faecium BFE 900.";
Appl. Environ. Microbiol. 65:2170-2178(1999).
EMBL; AF121254; AAD28228.1;
                                                                                                                                                           Enterococcus faecium (Streptococcus faecium).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9AECD1C6BF2DEC9C CRC64;
                                                                             01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BETA-GLUCOSIDE SPECIFIC TRANSPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 433.5; DB 2; 35.1%; Pred. No. 6.9e-19; ive 62; Mismatches 130;
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                   618 AA
                                                          Created)
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01-JUN-2001 (TrEMBLrel. 17, Created)
                   PRT;
                                                                                                                                                                                                                                                                                    STRAIN=BFE 900;
MEDLINE=99240446; PubMed=10224016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD002243; PTS_EIIA; 1.
PROSITE; PS0031; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CXS; SEQUENCE 618 AA, 67051 WW; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P20166; 1AX3.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00358; PTS_EIIA_1; 1.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
                                                            (TrEMBLrel. 12,
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                   PRELIMINARY;
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=1352;
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                                                        01-NOV-1999
01-NOV-1999
                                      09X565
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Q99RQ0
ID Q99RQ0
AC Q99RQ0;
DT 01-JUN
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                   09X565
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09X565
                     HODEN DE LE LE DE 
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SERAIN=EL TOR N16961 / SEROTYPE 01;
STRAIN=EL TOR N16961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Meldelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
McDonald L., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Kuroda M., Ohta T., Ochiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AFFKVKAIALGTAGLPGFISINPVHAGWLHYFVGMTISFII----AITVTLILSKRKAN 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 ALFNIKAVALGAAGFLGVVSIDA--PDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 AA; 51232 MW; D88607F6E0AF2E84 CRC64;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
SUCROSE-SPECIFIC IIBC COMPONENT.
                                                                      update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT.
                                                                                                                                                          Staphylococcus aureus subsp. aureus N315.
Bacteria; Firmicutes; Bacillus/Klostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.0%; Score 418.5; DB 2;
49.7%; Pred. No. 4.1e-18;
live 32; Mismatches 47;
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InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lancet 357:1225-1240(2001).
EMBL; AP003137; BAB43469.1;
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01-JUN-2001 (
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                                                                                                                      4; Gaps
                                                                                      Ouery Match
22.8%; Score 416; DB 2; Length 479;
Best Local Similarity 52.4%; Pred. No. 5.8e-18;
Matches 86; Conservative 26; Mismatches 48; Indels
Pfam; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Complete proteome.
SEQUENCE 479 AA; 50292 MW; DC0E129229957E3C CRC64;
                                                                                                                                                                                                                                                                  117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 160
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March 21, 2002, 16:28:49 ; Search time 17.08 Seconds
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US-09-604-231-4 1821 Title: Perfect

1 YDFGGPVGGLLFGLVYSPIV.....IEAGANLLNVAKKEAVPATP 362 score: Sequence:

Scoring table:

100059 seqs, 36664827 residues , Gapext 0.5 BLOSUM62 Gapop 10.0 , Searched:

100059 hits satisfying chosen parameters: Total number of

DB seq length: 0 DB seq length: 200000000 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CTIMMADIES

	Description	P12655 streptococc	470	o.	-	P08722 escherichia	8	Q9cjz2 pasteurella	325		_	P45604 klebsiella			P08470 salmonella	č	ຶ່		0	P39816 bacillus su	0	P50829 bacillus su		P45618 mycoplasma	Ö	7		P45338 haemophilus	vxi7		3	P75569 mycoplasma	7315	P24241 escherichia
SUMMARIES	ID	PTSA STRMU	PTSA_PEDPE	PTBA_BACSU	PTBA_ERWCH	PTBA_ECOLI	PTSB_STAXY	PTSB_PASMU	PTSB_VIBAL	PTGA_CORGL	PTTB_BACSU	PTAA_KLEPN	PTSB_BACSU	PTGA_BACSU	PTSB_SALTY	PTAA_ECOLI	PTGA_BACST	PTSB_KLEPN	SACX_BACSU	YBFS_BACSU	PTGA_BORBU	YPQE_BACSU	LACY_STRTR	PTGA_MYCCA	PTTB_ECOLI	PTGA_ECOLI	PTGA_SALTY	PTGA_HAEIN	PTGA_BUCAI	RAFP_PEDPE	LACY_LACDE	PTGA_MYCPN	PTGA_MYCGE	PTDA_ECOLI
	Length DB	664 1			631 1			474 1	479 1	674 1	470 1	651 1	460 1	699 1	456 1	648 1	324 1	456 1	459 1	631 1	189 1	168 1		154 1								940 1	908 1	485 1
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EMBL; M22711; AAA26971.1; -. EMBL; D13175; BAA02466.1; -.

34 161.5 8.9 482 1 PTSB_VIBCH 35 157.5 8.6 639 1 LACY_LEULA 37 115.5 6.3 538 1 TCMA_STRGA 38 113.5 6.2 1179 1 CIND_BACTA 40 109 6.0 1951 1 CIND_BACTA 41 107.5 5.9 2249 1 OMPA_RICRI 42 104 5.7 451 1 PTCC_BACST 43 104 5.7 577 1 PTCC_BACST 44 101.5 5.6 413 1 FABF_VIBCH 45 101.5 5.6 1654 1 OMPB_RICRI	-	Q48624 leuconostoc P77272 escherichia	P39886 streptomyce								Q53047 r outer mem
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66666666666666666666666666666666666666	161.5	157.5	115.5	113.5	110	109	107.5	104	104	101.5	101.5
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUGAR PHOSPHOTARNSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
TRANSPORT SYSTEM. THE ITCD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHORHEY; IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.;
"Isolation, characterization and sequence analysis of the scrK gene encoding fructokinase of Streptococcus mutans.";
J. Gen. Microbiol. 139:921-927(1993).
-i. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
                                                                           01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC INABC COMPONENT (EINABC-SCR) (SUCROSE-PERMEASE INABC COMPONENT) (FIGSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                Sato Y., Poy F., Jacobson G.R., Kuramitsu H.K.; "Characterization and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans phosphoenolpyruvate-dependent sucrose phosphotransferase system."; J. Bacteriol. 171:263-271(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILB DOMAIN.
-:- SIMILARITY: CONTAINS A PTS EILD DOMAIN.
                                       664 AA
                                                                                                                                                                                                                                                                                                                                                         STRAIN=GS-5;
MEDLINE=89123027; PubMed=2536656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93329360; PubMed-8336109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 639-664 FROM N.A.
                                         STANDARD;
                                                                                                                                                                                                                               Streptococcus mutans
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                                                                                                                                                                                                                                                                        Streptococcus
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                                    PTSA_STRMU P12655;
RESULT 1
PTSA_STRMU
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. SCR) (SUCROSE-SPECIAL SCR)
15-JUL-1999 (Rel. 32, 7.1.69) (Rel. SCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pediococcus pentosaceus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL---FNQG---GSFIFATASMANIAQ
                                                                                                                                                                                                                                                                                                                                 115 IALFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID
                                                                                                                                                                                                                                                                                                                                                         PDATAAPVPAGTTKAEAEAPAEFSNDST-----IIQAPLTGEAIALSSVSDAMFASGK
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                                                                                                                                                      (BY SIMILARITY). (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                             Length 664;
                                                                                                                                                                                                                              116; Indels
                                                                     Probom; PD001476; PTS_EIIB; 1.
Probom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
PROSPROGRAGEARS system; Sugar transport; Transferase;
Phosphorylation; Transmembrane.
                                                                                                                                                                                  809E63E32281A9A1 CRC64;
                                                                                                                                                                                                          39.0%; Score 711; DB 1;
42.1%; Pred. No. 3.8e-43;
tive 73; Mismatches 116,
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      HSSP; P08837; ZF3G.
InterPro; IPR001127; PTS_BIIA.
InterPro; IPR001996; PTS_BIIB.
InterPro; IPR03352; PTS_BIIC.
Pfam; PF00356; PTS_BIIB. 1.
Pfam; PF00357; PTS_BIIB; 1.
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664 AA;
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SEQUENCE FROM N.A.
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P43470;
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Leenhouts K.E.J., Bolhuis A.A., Kok J.J., Venema G.G.;
Submitted (XXX-1994) to the EMBL/Genbank/DDBJ databases.
-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
-2- SUGAR PHOSPHOTRANSFERALES SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM THE IICD DOMAINS CONTAIN THE SUGAR BINDING: STTE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
C87BA09D550A77F8 CRC64;
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                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-1- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-1- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126;
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EIIC DOMAIN.
EIIA DOMAIN.
PHOSPHORYLATION (
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HSSP: P20166; LAX3.
InterPro: IPR001127; PTS_EIIA.
InterPro: IPR001127; PTS_EIIA.
InterPro: IPR001352; PTS_EIIB.
InterPro: IPR003352; PTS_EIIB.
InterPro: IPR00356; PTS_EIIB.
Pfam; PF00358; PTS_EIIB.
I.
ProDom; P0001476; PTS_EIIB; I.
ProDom; P0002243; PTS_EIIB; I.
PROSITE; PS00371; PTS_EIIA.; I.
PROSITE; PS00371; PTS_EIIA.; I.
PROSITE; PS01035; PTS_EIIB.; I.
PROSITE; PS01035; PTS_EIIA.; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOI. Gen. Genet. 250:761-766(1996).

-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS CONTAINT THE SUGAR BINDING SITE AND THE TRANSMEBREANE CHANNEL; THE IIA DOMAIN THE PENARM PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                         DEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL--LNVAK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Now beta-glucoside (bg1) genes in Bacillus subtilis: the bg1P gene product has both transport and regulatory functions similar to those of Bg1F, its Escherichia coli homolog.";

Bacteriol. 177:1527-1535(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168 / BGSC1A1;
MEDLINE-95219088; PubMed-7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
                                                                                                                                                                                                                                                                                                                                                                                         (EIIABC-BGL)
                                                                                                                                                                                                                                                                                   P40739; 045661;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-BC (BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-168;
MEDLINE-96204517; PubMed-8628237;
Beloin C., Hischbein L., le Hegarat F.;
"Suppression of the B91+ phenotype of a delta hns strain of Escherichia coli by a Bacillus subtilis antiterminator binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                  609 AA
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MEDLINE=95189730; Pubmed=7883710;
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                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                           649
                                                                                           355 KEAVPAT 361
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                                                                                                                                           643 ASSVAAT
                                                                                                                                                                                                                                                                  PTBA_BACSU
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PTBA_BACSU
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60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 IKAVALGA-AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENTINGENAGLIPSIPVFIGPTFIYAMIGLVIAFAAETAAAYLLGFEDVPSDGS-----
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SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                          Inter.

Pfam; PP0035b; ._

Pfam; PP0037; PTS_EIIb; ..

R Probom; PD001476; PTS_EIIB; 1.

DR PROSITE; PS00371; PTS_EIIB; 1.

DR PROSITE; PS00371; PTS_EIIB_1: 1.

DR PROSITE; PS01035; PTS_EIIB_1: 1.

DR PROSITE; PS01035; PTS_EIIB_1: 1.

RW Phosphoryalation; Transmembrane; Complete proteome.

RW Phosphoryalation; Transmembrane; Complete proteome.

All EIIB DOMAIN.

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Pred. No. 2.6e-29;
3; Mismatches 142; Indels
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POTENTIAL.
POTENTIAL.
L -> F (IN REF. 2).
E -> G (IN REF. 2).
G -> HR (IN REF. 2).
DG -> HR (IN REF. 2).
I -> M (IN REF. 2).
G -> G (IN REF. 2).
G -> S (IN REF. 2).
G -> S (IN REF. 2).
SF6330C671D21FBBD CR.
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                                                                                                                                                           SUBCLILE, CONTROLLEY, PTS. EIIA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIB.
Pfam; PF00358; PTS_EIIA_1; 1.
Pfam; PF00357; PTS_EIIA_1; 1.
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                                          EMBL; X85408; CAA59697.1; --
EMBL; 299124; CAB15963.1; --
PIR; S47174, S47174.
HSSP; P20166; LAX3.
Subtilist; BG10934; bg1P.
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Best Local Similarity 33.28
Matches 121; Conservative
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Matches 123; Conservative
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631 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-912114; Pubmed-1732212;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chippaux M., Barras F.;
el Hassouni M., Henrissat B., Chipani control beta-glucoside
utilization in Erwinia chrysanthemi: comparison with the Escherichia
coli bgl operon and evidence for a new beta-glycohydrolase family
including enzymes from eubacteria, archeabacteria, and humans.";
J. Bacteriol. 174:765-777(1992).

1. Bacteriol. 174:765-777(1992).

2. Bacteriol. 174:765-777(1992).

2. Bacteriol. TASSPERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMANNS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONAIN WHICH FINALLY TRANSFERS IT TO
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-:- SIMILARITY: CONTAINS A PIS BIIA DOMAIN.
-:- SIMILARITY: CONTAINS A PIS BIIB DOMAIN.
-:- SIMILARITY: CONTAINS A PIS BIIC DOMAIN.
                                                                                                                                                                                                                                                        (EIIABC-BGL)
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                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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R HSSP, P20166; JAX3.

R HSSP, P20166; JAX3.

R InterPro; IPR001127; PTS_EIIA.

DR InterPro; IPR001305; PTS_EIIA.

DR Pfam; PF00378; PTS_EIIA.

DR PF000578; PTS_EIIA.

DR PF00000; PD001476; PTS_EIIE; 1.

DR PF00000; P5000717; PTS_EIIA; 1.

DR PROSITE; PS000717; PTS_EIIA; 1.

DR PROSITE; PS01035; PTS_EIIA.

DR PROSITE; PS01035; PTS_EIIA.

DR PROSPHOCYPLAION; TTS_EIIA.

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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC ITABC COMPONENT (EIIABC-BC
(BETA-GLUCOSIDES-PERMEASE ITABC COMPONENT) (PHOSPHOTRANSFERASE
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                                                                                                                                                631 AA
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                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                            Erwinia chrysanthemi
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P26207;
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20-AUG-2001 (Rel. 40, Last sequence update)
PTS SYSTEM, BETA-GLUCOSIDES-SPECIFIC IIABC COMPONENT (EIIABC-BGL)
(BETA-GLUCOSIDES-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-BGL).
BGLF OR BGLS OR B3722.
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Bramley H.F., Kornberg H.L.;
"Nucleotide sequence of bglC, the gene specifying enzymeIIbgl of
PEP:sugar phosphotransferase system in Escherichia coli K12, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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PHOSPHORYLATION (BY SIMILARITY).
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MEDLINE-88009877; PubMed=3309161;
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                                                                                                                                                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE. SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
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Probom; Processor, Proces
                                          Schnetz K., Toloczyki C., Rak B.;
Beta-glucoside (bgl) operon of Escherichia coli K-12: nucleotide
"Sequence, genetic organization, and possible evolutionary
relationship to regulatory components of two Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ON BGLG.
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FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON BG
CATALYTIC CATIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
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                      MEDLINE-8722180; Pubmed=3034860;
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InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001196; PTS_EIIB.
InterPro; IPR001352; PTS_EIIC.
Pfam; PF00158; PTS_EIIA_1; 1.
Pfam; PF00378; PTS_EIIB; 1.
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PIR; C25977; C25977.
PIR; A47616; A47616.
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"Cloning and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system from stephiylococcus xylosus.";

Mol. Gen. Genet. 241:33-41(1993).

-! FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 35, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC. 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                               128 AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD-ATAAPVPAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 PSIFTFMQTIPSTGIDFTVWASV----IGGVIAIGCAFV---GTVMLHFITAKRQPAQG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                              GLLFGLVYSPIVITGLHQSFPPIELELFN-QGGSFIFATASMANIAQGAACLAVFFLAKS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR -
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-:- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 APQEKTPEVITPPEQGGICSPWTGEIVPLIHVADTTFASGLLGKGIAILPSVGEVRSPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 TKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS
                                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                        Length 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEDIPAIREAGEPLITPVLISNSDDFTDVLPHGTAQISAGEPLLSIIR 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                                                     ; Score 450; DB 1; Length 62; Pred. No. 1.1e-24; 64; Mismatches 154; Indels
                                                                                                                                                             9E12A2207125C4E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus xylosus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑĄ
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                              POTENTIAL
                                                    POTENTIAL
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  POTENTIAL
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MEDLINE-94049686; PubMed-8232209;
                                                                                                                                                                ₹
                                                                                                                                                                                                                                     24.7%;
33.3%;
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3%
Matches 116; Conservative
                                                                                                                                                                66482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
375
401
424
452
510
546
                                                                                                                                                             625 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
355
381
404
432
490
526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTSB_STAXY
P51184;
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PTSB_VIBAL P22825;
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MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                 DOMAIN
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 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

1. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE TRANSPORT SYSTEM. THE IICD DOMANNS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-BERNARSE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
SCRA OR PTSB OR PM1846.
                                                                                                                                                                                                                                                                                                                                                                                              ACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                  1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 ALFNIKAVALGAAGFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                     ELIC DOMAIN.
PHOSPHORITATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
ABABID9785D84E47 CRC64;
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE SUGAR (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR
                                                                                                                                                                                                                                                                                                                                                         47; Indels
                                                                                                                                                                                                                   Transferase;
                                                                                                                                                                                                                  Phosphotransferase system; Sugar transport; Tra:
Transmembrane; Inner membrane; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                24.5%; Score 446.5; DB 1
52.5%; Pred. No. 1.4e-24;
ive 30; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 AA
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN
                                                                                                                                                                                                                                            EIIB DOMAIN
                                                                                                                                                                                      ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-PM70;
MEDLINE-21145866; Pubmed-11248100;
                                                                                                                                      InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
                                                                                                                                                                                                                                                                                            51326 MW;
                                                                                                                          EMBL; X69800; CAA49461.1;
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.59
Watches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                     480
26
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida
                                                                                                                                                                                                                                                                                          480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   26
325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTSB_PASMU
                                                                                                                                                                                                                                                     DOMAIN
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9CJZ2;
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransferase; Sugar transport; Plasmid;
ler membrane; Phosphorylation; Complete protecome.
Possible powaln.
Portervial.
Portervial.
Portervial.
202 POTERVIAL.
249 POTERVIAL.
249 POTERVIAL.
249 POTERVIAL.
249 POTERVIAL.
249 POTERVIAL.
249 POTERVIAL.
23 POTERVIAL.
23 POTERVIAL.
23 POTERVIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YDFGCPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ----GGSFIFATASMANIAQGA 56
                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Protéobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_raxID-663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
D26FA1A059603C01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||:||:||||| |: || : || : || : |
|LFNVKAIALGAAGLPGIPSIKPDSLAMYCVGMLISASIAFTLIVILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.0%; Score 418; DB 1; 50.9%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 AA
                                                                               SIMILARITY: CONTAINS A PTS EIIB DOMAIN. SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006222; AAK03930.1; -.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfan; PF00367; PTS_EIIB; 1.
Pfan; PF02378; PTS_EIIC; 1.
PROSITE; PS01035; PTS_EIIB_CYS; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphotransferase system; Transferase;
PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio alginolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324
474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 85; Conserv
                                                        (BY SIMILARITY
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä;
                                                                                                    repressor-encoding gene (SCTR).";
Gene 101.45-50(11991).
-1-FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL, THE IIA DOMAIN CONTAINS THE PRIMARY
PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR): IIA TRANSFERS ITS
PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
latch G.L., Scholle R.R., Woods D.R.; Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                          CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIL DOMAIN.
                                                      SEQUENCE OF 1-12 FROM N.A. MEDLINE-91285433; PubMed-2060795; Blatch G.L., Woods D.R.; "Nucleotide sequence and analysis of the Vibrio alginolyticus scr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY SIMILARITY). PHOSPHORYLATION (BY SIMILARITY). FBF906B5170E3EB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCA-VVTFFIAFGAAIAYGL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00367; PTS_EIB; 1.
Pfam: PF00378; PTS_EIIC; 1.
Prodom; PD001476; PTS_EIIE; 1.
PROSITE; PS01035; PTS_EIIB; 1.
Phosphotransferase system; Sugar transport; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.6%; Score 412; DB 1; 49.7%; Pred. No. 3.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIIB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; M76768; AAA27555.1; -.
EMBL; M35009; AAA27557.2; -.
PIR; JQ0781; JQ0781.
HSSP; P05051; JIBA.
InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTGA_CORGL STANDARD;
Q45298;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49890 MW;
                        uptake-encoding region.";
Gene 95:17-23(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 22.6
Best Local Similarity 49.7
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 AA;
                                                                                                                                                                                               THE SUGAR.
  Blatch G.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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PTGA_CORGL
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                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence update)
20-AdG-2001 (Rel. 40, Last annotation update)
PIS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (GLUCOSE-PERMEASE IIABC COMPONENT) (FHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69) (EII-GLC/EIII-GLC).
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PHOSPHORYLATION (BY SIMILARITY).
67A75AAF76E42FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
-!- SUMCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacteriaceae,
                                                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
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POTENTIAL.
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ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS002243; PTS_EIIA; 1.
PROSITE; PS00131; PTS_EIIB_L1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MM;
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InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00358; PTS_EIIA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L18875; AAA22992.1; -.
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364
397
429
462
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-ATCC 13869;
                                                                                                                                                                                                                                      Corynebacterium.
NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
                                                                                                                                                                        Plasmid pBSBG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE SUGAR.
                                                                                                                                                                                                                                                                                                                                                   Yoon K.-H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 QTNNTPAAPAAPVAPAAGAAAGGAAGAT-AVATKPRLAAGQLVEITSPLEGHAVPLSEV 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | | | | :: :||||: | | | : |:: | :|||| | | | : |:: ||:|||| | | : |:: ||:||| | | : |:: ||::||| | | : |:: ||::||| | | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||::||| | : |:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: ||:: |
                                                                                                                                                                                                          307 IVIPLLYPFLVPLGLHWPLNAIMIQNLNTLGYDFIQGPMGAWNFACFGLVTGVFLIALKE 366
                                                                                                                                                                                                                                                                          69 KLKGLAGAS--GVSAVL--GITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 FDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F---VFTSLLTIPAMDPWLGYTVGIAAAF--FTSMLLVLFFDYRSDAERDEAKAQMAAAE 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoeck F., Dahl M.K.;
"Analysis of DNA flanking the treA gene of Bacillus subtilis reveals genes encoding a putative specific enzyme IITre and a potential regulator of the trehalose operon.";
Gene 175:59-63(1996).
                                                                      Gaps
                                                                                                                                      10 LLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLAKSE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes for trehalose metabolism and acetoin utilization.";
Microbiology 142:3057-3065(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTTB_BACSU STANDARD; PRT; 470 AA. P9794; 034771; 01-FEB-1995 (Rel. 31, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 20-AG-2001 (Rel. 40, Last annotation update) PROBABLE PTS SYSTEM, TREHALOSE-SPECIFIC IIBC COMPONENT (EIIBC-TRE) (TREHALOSE-PERMEAE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, COMPONENT) (EC 2.7.1.69) (EII-TRE).
                                                                                                                                                                                                                                                                                                                                                                                                                125 LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PDATAAPV-----PAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSV
                                                                      41;
   Length 674;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.NCBI_TaxID=1423;
   DB 1;
                                                                   61; Mismatches 156;
                                   6e-20;
21.2%; Score 386.5; 31.0%; Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=168 / MARBURG;
MEDLINE=97074649; PubMed=8917076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97417488; PubMed-9272861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97124190; PubMed=8969503;
                                                                   Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : | : : |
657 EAAQADATTTVIKV 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 GLGEIEAGANLLNV 352
                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TREP OR TREB.
Bacillus subtilis.
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   Query Match
                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                427
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                                                                                                                                 Helfert C., Gotsche S., Dall M.K.;
"Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed by a phospho-alpha (1-1)-glucosidase encoded by the treA gene.";
Mol. Microbiol. 16:111-120(1995).

I. FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE—TRANSPORT SYSTEM. THE IICD DOMAINS COMTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
Bacillus subtilis genome reveal genes for a new two-component
three spore germination proteins, an iron uptake system and
stress response protein.";
                                                                                                                                                                                                                                                                                                                      -i- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR -
PROPEIN HISTIDINE + SUGAR PHOSPHATE.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
-i- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-i- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIIB DOMAIN.
EIIC DOMAIN.
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 18.1%; Score 330; DB 1; Length 470; Best Local Similarity 41.6%; Pred. No. 2.4e-16; Matches 67; Conservative 34; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Phosphotransferase system; Sugar transport; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F -> S (IN REF. 1).
M -> L (IN REF. 1 AND 4).
A -> G (IN REF. 1 AND 4).
7A741850A2697D53 CRC64;
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POTENTIAL.
POTENTIAL.
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                                                                                                                      MEDLINE=95379486; PubMed=7651129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 254245; CAA91014.1; --
EMBL, D83967; BAA22409.1; --
EMBL, D86417; BAA22289.1; --
EMBL, X80203; CAA56494.1; --
EMBL, Z99108; CAB12609.1; --
HSSP; P05653; 11BA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001996; PTS_EIIB.
InterPro; IPR003352; PTS_EIIC.
Pfam; PF00367; PTS_EIIB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
                                                                                         SEQUENCE OF 324-470 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02378; PTS_EIIC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49999
        Bacillus subtilis
                                                        Gene 194:191-199(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          363
465
470 AA;
                         system, three s
qeneral stress
                                                                                                                                                                                                                                                                                                          SUGAR.
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TRANSMEM
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOI. Gen. Genet. 230:270-276(1991).
-!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE -TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS IT TO PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC COMPONENT (EIIABC-NAG)
N-ACETYLGLUCOSAMINE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-NAG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
                                       65 AKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparison of the sequences of the nagE operons from Klebsiella pneumoniae and Escherichia coll K12: enhanced variability of the enzyme IIN-acetylglucosamine in regions connecting functional
                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphotransferase system; Sugar transport; Transferase; Phosphorylation; Transmembrane; Inner membrane.
                                                                                                LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLY 165
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SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                                                  651
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MEDLINE=92079906; Pubmed=1745234;
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Probom; PD002243; PTS_EIIA; 1.
PROSITE; PS00371; PTS_EIIA_1; 1.
PROSITE; PS01035; PTS_EIIB_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001127; PTS_EIIA.
Interpro; IPR001996; PTS_EIIB.
Interpro; IPR003352; PTS_EIIC.
Pfam; PF00358; PTS_EIIA_1; 1.
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                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                               pneumoniae
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P45604;
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01-NOV-1988 (Rel. 09, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC 2.7.1.69) (EII-SCR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 YIAAVGGTDNLKAIDACITRLRLTVGDSAKVNDAACKRLGASGVVKLNKQTIQVIVGAKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 LLYLLHAVLTGISLFIATALGIHAGFSFSAGAIDYVLMYSLPAA-----SK
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                                 SIMILARITY).
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PHOSPHORYLATION
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A Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
A Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
A Hullo M.F., Ionescu M., Lubochinsky B., Marcellno L., Moszer I.,
A Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
A Rapoport G., Danchin A.;
A Rapoport G., Danchin B.;
A Rapoport G., Danchin G., The PHOSPHORNOLPPRUVATE-DEPENDENT G. TRANSPORT SYSTEM, THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEBRARE SCYEM (PTS), A MAJOR CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DOMOR IS PHOSPHORYLATION SITE (THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR = PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLOLAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
SIMILARITY: 57% IDENTITY WITH THE NEGATIVE REGULATORY PROTEIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: ACTS AS BOTH A KINASE AND A PHOSPHATASE ON SACT (BY
                                                                                  SEQUENCE FROM N.A.
MEDILINE-88097369; PubMed-3122206;
MEDILINE-88097369; PubMed-3122206;
"Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coll and homology to enzymes II from enteric bacteria"; proc. Natl. Acad. Sci. U.S.A. 84:8773-8777(1987).
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PHOSPHORYLATION (BY SIMILARITY)
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DOMAIN

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EIIC DOMAIN.
                 Bacteria; Firmicutes; Bacillus/Clostridium group;
                            Bacillus/Staphylococcus group; Bacillus.
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60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EIIABC-GLC) (GLUCOSE
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                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTGA_BACSU STANDARD; PRT; 699 AA. P20166; P08875; 01-NOV-1988 (Rel. 09, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 01-DEC-1992 (Rel. 40, Last annotation update) PTS SYSTEM, GLUCOSE-SPECIFIC IIABC COMPONENT (EIIABC-GLC) (GLUCOMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC COMPONENT) (EC 2.7.1.69) (EII-GLC/EIII-GLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and nucleotide sequence of the ptsG gene of Bacillus
                                                                                                                                                                                                                        Length 460;
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MEDLINE-92001991; PubMed~1911744;
Liao D.-I., Kapadia G., Reddy P., Saier M.H. Jr., Reizer
                                                                                                                                     6A303DC042BFE379 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 IKAVALGAAGFLGVVSIDAP----DMVMFL----VCAVVTFFIAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | | : :::| || : :::| || 405 VAANAYGLTG-IPMIAIAAPFGFSNLIHYLIGMAIAAVSAFIAAF 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                  16.7%; Score 305; DB 1;
44.8%; Pred. No. 1.4e-14;
Live 25; Mismatches 56
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STRUCTURE BY NMR OF EIIA DOMAIN.
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                                                                                                                                                                                                                                                                           Conservative
348
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                                                                                                                                                      MEDLINE-91299743; PubMed-1906345; Fairbrother W.J., Cavanagh J., Dyson H.J., Plamer A.G. III, Sutrina S.L., Reizer J., Saier M.H. Jr., Wright P.E.; Polypeptide backbone resonance assignments and secondary structure of Bacillus subtilis enzyme IIIglc determined by two-dimensional heteronuclear NMR spectroscopy.";
                                                                                                           CATALTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR PROTEIN HISTIDINE + SUGAR PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
SIMILARITY: CONTAINS A PTS EIB DOMAIN.
SIMILARITY: CONTAINS A PTS EILB DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AACLAVFFLAKSEKLKGLAGASGVSA----VLGITEPAIF
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                                                         01-AUG-1988 (Rel. 08, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PTS SYSTEM, SUCROSE-SPECIFIC IIBC COMPONENT (EIIBC-SCR) (SUCROSE-PERMISASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT)
(EC. 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                          "DNA sequence of the gene scrA encoding the sucrose transport protein EnzymaII(Scr) of the phosphotransferase system from enteric bacteria: homology of the EnzymeII(Scr) and EnzymeII(Bgl) proteins."; Mol. Microbiol. 2:9.17(1988).
                                                                                                                                                                                                                                                                                                                                             Jahreis K., Lengeler J.W.; "Molecular analysis of two ScrR repressors and of a ScrR-FruR hybrid repressor for sucrose and D-fructose specific regulons from enteric bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.-!- SIMILARITY: CONTAINS A PTS EIIB DOMAIN.
-!- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                      456 AA.
                                      PRT;
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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-88216186; Pubmed-3285123;
Ebner R., Lengeler J.W.;
                                                                                                                                                                                                                                                                                                                                 MEDLINE-94018607; PubMed-8412665;
                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 9:195-209(1993).
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                                     STANDARD;
                                                                                                                                               Salmonella typhimurium.
Plasmid pUR400.
                                                                                                                                                                                               NCBI_TaxID=602;
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                                   PTSB_SALTY
P08470;
                                                                                                                                                                                   Salmonella.
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PTSB_SALTY
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MEDLINE-88212176; PubMed-3284790; Rogers M.J. Ohgi T., Plumbridge J., Soell D.; Rogers M.J. Ohgi T., Plumbridge J., Soell D.; the Squences of the Escherichia coli nagE and nagB genes: the structural genes for the N-acetylglucosamine transport protein of the barterial phosphoenolpyruvate: sugar phosphotransferase system and for glucosamine-6-phosphate deaminase."; ene 62:197-207(1988).
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01-MAR-1989 (Rel. 10, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
PTS SYSTEM, N-ACETYLGLUCOSAMINE-SPECIFIC IIABC COMPONENT (EIIABC-NAG)
N-ACETYLGLUCOSAMINE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE
ENZYME II. ABC COMPONENT) (EC 2.7.1.69) (EII-NAG).
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STRAIN-KIZ. / MG1655,
STRAIN-KIZ. / MG1655,
Pubbed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
Probom; PD001476; PTS_EIIB; 1.
PROSITE; PS01035; PTS_EIIB, 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
PROSIDE; PS01055; PTS_EIIB_CYS; 1.
Transmembrane; Inner membrane; Phosphorylation.
DOMAIN 1. ? EIIB DOMAIN.
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PHOSPHORYLATION (BY SIMILARITY).
98A6F1620AE50885 CRC64;
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                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAI 160
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MEDLINE-89050950; Pubmed-3056518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 27:6054-6061(1988).
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356 AA;
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Matches 64; Conserv
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DOMAIN
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PTAA_ECOLI
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1E24C97CFCBBAA59 CRC64;

68346 MW;

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Search completed: March 21, 2002, 16:28:51 Job time: 331 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DR HSSP; P08837, 2F3G.
DR HSSP; P08837, 2F3G.
DR ECGEne; EG10635; nagE.
DR InterPro: IPR001396; PTS_EIIA.
DR InterPro: IPR001396; PTS_EIIA.
DR InterPro: IPR001395; PTS_EIIA.
DR Pfam; PP00378; PTS_EIIB: 1.
DR ProDom; PD001476; PTS_EIIB: 1.
DR ProDom; PD001476; PTS_EIIB: 1.
DR ProDom; P000378; PTS_EIIB: 1.
DR ProSTE; PS00371; PTS_EIIA: 1.
DR PROSTE; PS01037; PTS_EIIA.
TRANSMEMBRANE: SUBSECTION TRANSFERSE;
TRANSFERSE SYSTEM: STANSFERSE;
TRANSFERSE SYSTEM: STANSFERSE SYSTEM: STANSFERSE;
TRANSFERSE SYSTEM: STANSFERSE SYSTEM: STANSFERST
                                                                                                                                                                                                                                            DNA Res. 3:137-155(1996).

-1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE -TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
                                                                              Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Maranta K., Nashimoto H., Nishio Y., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;

Yano M., Horiuchi T.;

An 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                         THE SUGAR.

CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOHISTIDINE + SUGAR =
PROTEIN HISTIDINE + SUGAR PHOSPHATE.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
SIMILARITY: CONTAINS A PTS EIIA DOMAIN.

SIMILARITY: CONTAINS A PTS EIIC DOMAIN.

SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
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                                                        MEDLINE-97061202; PubMed-8905232;
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EMBL; AE000171; AAC73773.1; -.
EMBL; D90770; BAA35322.1; -.
PIR; B29895; WQEC2N.
PIR; A28896; A28896.
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                                                                                                                                      ------GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163
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                                                           Gaps
                                                                                                        5 GPVGGLLFGLVYSPIVITGLHQSFPPI-------ELELFNQG----GSF 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF : : : : | | | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 -PVAAASAEATP-ATAAPVAKPQAVPNAVSIAE-----LVSPITGDVVALDQVPDEAF
                                                                                                                                                                                                            43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF-----
                                                   62; Mismatches 162; Indels 154;
                                                                                                                                                                                                                                                                                                                  ------GVNLRLRWPFFIGIGTAAIGGAL--------GVNLRLRWPFFIGIGTAAIGGAL
Score 295; DB 1; Length 648; Pred. No. 1e-13;
     16.2%;
23.2%;
  Query Match 16.2%
Best Local Similarity 23.2%
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAGANLLNVAKK 355
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

US-09-604-231-4 1821 1 YDFGGFVGGLLFGLVYSPIV.....IEAGANLLNVAKKEAVPATP 362 Title: Perfect score: Sequence:

Scoring table:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pirl:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	phosphotransferase	feras	PTS system, beta-q	system, beta-	phosphotransferase	beta-qlucoside per	-	Þ	phosphotransferase	hypothetical prote		PTS system, sucros	sucrose uptake pro	PTS system, trehal	phosphotransferase	hypothetical prote	phosphotransferase	phosphotransferase	PTS system, sucros	phosphotransferase	phosphotransferase	phosphotransferase	hypothetical prote	44	sac operon requiat		PTS system, glucos	insucrase	D.
SUMMARIES	QI	224	S44257	нв3686	C83724	868599	140406	T47097	B42603	C25977	D86807	S39978	F82432	JQ0781	н83926	C69725	D86766	S46953	S18607	H83881	A39938	WQBSGS	DEC 2	E85567	S62331	I39868	WQEBST	D83755	JU0293	C83839
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	Score	711	706.5	562.5	550.5	515.5	515	503	492.5	450	448	446.5	416		350.5	330		313.5	313	310	305	299	295	294	293.5	290	277.5	276	273	271.5
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phosphotransferase phosphotransferase	phosphotransferase	phosphotransferase	lactose transport	phosphotransferase	phosphotransferase	PTS system, glucos	PTS system, glucos	phosphotransferase	PTS system, trehal	PTS system enzyme	phosphotransferase	phosphotransferase	probable phosphotr	raffinose carrier
D69750 S46952	F70169	H69940	A32241	C65236	WQECP3	D85884	G82257	WQEB3T	B82263	A86122	G64137	B84937	C83177	844253
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14.9			13.9	13.7	13.5	13.5	13.5	13.4						12.1
	14.1	14.0							13.4		13.1	12.7	12.4	221 12.1

## ALIGNMENTS

RESULT 1  Bigglin 10-Sep-1999  Figlin 10-Sep-
Insterase system enzyme II (EC 2.7.1.69), sucrose-specific -; Streptococcus mutans obsep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 #sequence_coccus mutans obsep-1999 #text_change 10-Sep-1999 #sequence_coccus mutans of the scrape in 171, 263-271, 1989 #text_change in 171, 263-271, 1989 #text_change in 171, 263-271, 1989 #text_change in 271, 271, 263-271, 1989 #text_change in 271, 271, 271, 271, 271, 271, 271, 271,

Length Indels

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PTS system, beta-glucoside-specific enzyme II, ABC component bglP [imported] - Bacill C:Species: Bacillus halodurans
C:Species: Bacillus halodurans
C:Species: Ol-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
C:Accession: C83724
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83550; MUID:20263314
A;Reference number: A83550; MUID:20263314
A;Reference number: A83550; MUID:20263314
A;Reference number: A83550; MUID:20263314
A;Reference number: A83550; MUID:20263314
A;Residues: 1-636 <ATC>
A;Residues: 1-636 <ATC>
A;Reperimental source: strain C-125
A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04314.1; GSPDB:G A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04314.1; GSPDB:G A;Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04314.1; GSPDB:G A;Genetics:
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C; Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 SVAVAPGAPGLLTIPIFYPEDGRGFVAFVIAIIISFVLA----AVLTYIVGFKDPVDDE 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 ATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
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                                                                                      30.9%; Score 562.5; DB 2; 34.6%; Pred. No. 1.8e-32; iive 78; Mismatches 143;
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                                                                                      Query Match 30.9%
Best Local Similarity 34.6%
Matches 124; Conservative
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Best Local Similarity 36.7%
Matches 132; Conservative
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C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000

C:Accession: H8366

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masul, N.; Fuji, F.; Hirra

Nucleic Acids Res. 28, 4317-4331, 2000

Nucleic Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20263314

A:Accession: H83686

A:Accession: H83686

A:Accession: Teferences: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04015.1; GSPDB:GNOG

C:Genetics:
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
C;Keywords: phosphotransferase
F;488-640/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol
                                                                                             pentos
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                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-651 <LEE>
A;Cross-references: EMBL:Z32771; NID:g493728; PIDN:CAA83668.1; PID:g475968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LFNIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.8%; Score 706.5; DB 2; 42.0%; Pred. No. 1.1e-42; iive 64; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.89
Best Local Similarity 42.09
Matches 154; Conservative
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A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Status: preliminary; nucleic acid sequence not shown; a.Status: DNA
A.Residues: 1-74, S', 76-182 <BEL>
A.Residues: 1-74, S', 76-182 <BEL>
A.Residues: 1-74, S', 76-182 <BEL>
A.Roszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fulita, M.; Fulita, K.; Fupidus, A.; Galizzi, A.; Galizzi, A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Rosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lu, H.; Masuda, S.; Mau A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lu, H.; Masuda, S.; Mau A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se Akuthors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se Akuthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Taesten, M.; Aritile: The complete genome sequence of the Gram-positive bacterium Bacillus subtill A. Accession: A69580; MUID:98044033
A.Accession: A69584
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: bglp
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
F;458-609/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
                                                                                                                                                                                            of Escherichia coli
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                                                                                                PIDN:CAA84286.1; PID:q505576
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                                                                                         A;Cross-references: EMBL:234526; NID:g505573; PIDN:CAA84286.1; PIR:Beloin, C.; Hirschbein, L.; le Hegarat, F.
Mcl. Gen. Genet. 250, 761-766, 1996
A;Title: Suppression of the Bgl+ phenotype of a Delta-hns strain A;Reference number: S65579; MuID:96204817
A;Accession: S65581
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Best Local Similarity
Matches 121; Conserv
                                    A; Molecule type: DNA
A; Residues: 1-609 <RES>
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C; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: L2-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 20-Jun-2000
C; Accession: 140406; S65581; A69594; S47174
R; Le Coq. D.; Lindner, C.; Kruger, S.; Steinmetz, M.; Stulke, J.
A; Title: New beta-glucoside (bg1) genes in Bacillus subtilis: the bg1P gene product has A; Reference number: 140404; MUID:95189730
A; Accession: 140406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAP 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                    |::|:| || || |: | | || |: |
521 EPSEGKLFSPVSGMVTALYPTHHALGITT----DRCAELLIHIGLDIVQLDGKFFTAHTI
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                                                                                                                                 QGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.3%; Score 515.5; DB 2; 36.3%; Pred. No. 3.9e-29; ive 63; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 36.3
Matches 128; Conservative
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A; Gene: arbF C; Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera F;479-631/Domain: phosphotransferase system glucose-specific enzyme II, factor III ho
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C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransfera
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A.Residues: 1-625 - GELAT>
A.Cross-references: GB:AE000449; GB:U00096; NID:g2367269; PIDN:AAC76745.1; PID:g17901
A.Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Reference number: A91833; MUID:87222180
A.Accession: C25977
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Kesidues: 1-625 < SCH>
A.Cross-references: GB:MI6487; GB:M60288; NID:g145414; PIDN:AAA23510.1; PID:g145418
R.Bramley, H.F.; Kornberg, H.L.
J. Gen. Microbiol. 133, 563-573, 1987
A.Tille: Nucleotide sequence of bglc, the gene specifying enzymeII(bgl) of the PEP:s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphotransferase system enzyme II (EC 2.7.1.69), beta-glucoside-specific - Escheri C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Jun-1999 C; Accession: C259,77, A47616; C55175 Fs. Schoetz, K.: Toloczyki, C.; Rak, B. J. Bacteriol. 169, 2579-2590, 1987 A; Title: Beta-glucoside (bgl) operon of Escherichia coli K-12: nucleotide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A47616
A;Status: preliminary
P;Retaus: preliminary
A;Molecule type: DNA
A;Residues: 1-625 <BRA>
A;Cross-references: GB:MI5746; NID:g145412; PIDN:AAA83837.1; PID:g145413
A;Cross-references: GB:MI5746; NID:g145412; PIDN:AAA83837.1; PID:g145413
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, N.A.; Rose, D.J.; Mau, B.; Sho, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Reference number: C65175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 YGLNSLLAGAVMGALWQVCVIFGLHWGFVPLMLNNFSVIGHDTLLPLLVPAVLGQAGATL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 IKAVALGAAGFLGVVSIDAPDMVMFLV-CAVVTFFIAFG-AAIAYGLYLVRRNGSIDPDA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574
                                                                                                                                                                                                                                                                                                                                                                                         1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 GVLLRTQDLKRKGIAGSAFSAAIFGITEPAVYGVTLPLRRPFIFGCIGGALGAAVMGYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 TAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGD
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                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                       62; Mismatches 154;
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                             27.0%; Score 492.5; DB 34.9%; Pred. No. 1.7e-27
                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.9%
Matches 123; Conservative
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C; Genetics:
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R;el Hassouni, M.; Henrissat, B.; Chippaux, M.; Barras, F.
J. Bacteriol. 114, 765-777, 1992
A; Title: Nucleotide sequences of the arb genes, which control beta-glucoside utilization olase family including enzymes from eubacteria, archeabacteria, and humans.
A; Recession: B42603
A; MUD: 92121114
A; Accession: B42603
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-61 < ELL>
A; Cross-references: GB: M81772; NID: g148385; PIDN: AAA24814.1; PID: g148387
A; Note: sequence extracted from NCBI backbone (NCBIN: 77535, NCBIP: 77537)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
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C;Species: Erwinia chrysanthem1
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                 conta
                                                                                                                                                                                C; Species: Bacillus subtilis
C; Date: 17 Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
C; Accession: T47097
R; Yoshida, K.; Sano, H.; Seki, S.; Oda, M.; Fujimura, M.; Fujita, Y.
Microbiology 141, 337-343, 1995
A; Title: Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome A; Reference number: Z24350; MUID:95219088
A; Reference number: Z24350; MUID:95219088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 IKAVALGA-AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 AAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 GQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDE 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG-SFIFATASMANIAQGAACL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 VASYIVGGNAGLPSIPVFIGPTFIYAMIGLVIAF--AAGTSAAYLL-----GFED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Mismatches 139; Indels
                                                                                                                                               hypothetical protein N17C [imported] - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.6%; Score 503; DB 2; 33.5%; Pred. No. 2.9e-28;
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C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: F82432
R; Heidelberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
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A;Residues: 1-479 <hr/>
A;Cross-references: GB:AE004395; GB:AE003853; NID:g9658068; PIDN:AAF96554.1; GSPDB:GN
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F82432
PTS system, sucrose-specific IIBC component VCA0653 [imported] - Vibrio cholerae (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the scrA gene encoding the sucrose-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Staphylococcus xylosus
C;Species: Staphylococcus xylosus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: S39978; E; Brueckner, R.
Mol. Gen. Genet. 241, 33-41, 1993
A;Title: Cloning and characterization of the scrA gene encoding the sucrose-A;Reference number: S39976; MUID:94049686
A;Accession: S39978
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X69800; NID:9407905; PIDN:CAA49461.1; PID:9407908 C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 ALFNIKAVALGAAGFLGVVSIDAPD--MVMFLVCAVVTFFIAFGAAIAYGLYLVRRN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 2
C;Superfamily: phosphotransferase system sucrose-specific enzyme II,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 24.5%; Score 446.5; DB 2; Similarity 52.5%; Pred. No. 2.2e-24; 93; Conservative 30; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
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52.4%; Pred. No. 3.2e-22;
iive 26; Mismatches 48;
                                                                                                                                                                                                                         296 GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                 scrA protein - Staphylococcus xylosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.48
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-480 <WAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                511
                                           236
                                                                                                                                                                                                                                                   267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dypothetical protein ptbA [imported] - Lactococcus lactis subsp. lactis (strain IL1403) (Species: Lactococcus lactis subsp. lactis C; Species: Je6607

R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli Genome Res. in press, 2001

A; Title: The complete genome sequence of the lactic acid bacterium.

A; Reference number: A86625

A; Accession: D86807

A; Accession: D86807

A; Accession: D86807

A; Reference number: A86625

A; Reference number: A86
C;Keywords: phosphoprotein; phosphotransferase; transmembrane protein F;473-625/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                      ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                          EKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPD-ATAAPVPAGT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSIFTFMQTIPSTGIDFTVMASV----IGGVIAIGCAFV---GTVMLHFITAKRQPAQG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 APQEKTPEVITPPEQGGICSPMTGEIVPLIHVADTTFASGLLGKGIAILPSVGEVRSPVA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGL---YLVRRNGSIDPDAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTMGA----GIFSFTSNITLTGEVSGAIKIMIVSAVAVIAGFVVTYLV----GFEDDVI 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAPVPAGTTKAEAEAPAEFSNDST---ILQAPLTGEAIALSSVSDAMFASGKLGSGVAIV 235
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                    9 GLLFGLVYSPIVITGLHQSFPPIELELFN-QGGSFIFATASMANIAQGAACLAVFFLAKS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 FGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQG-GSFIFATASMANIAQGAACLAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AQKKVVAGSAALISLFGIIEPAVYGVNLPRKYPFVIACISGALGATIIGYAQTKVYSFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKAEAEAPAEFSNDSTI1QAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVS
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                                                                                                                                             Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAK 354
                                                                                                                                                                                                               Indels
                                                                                                                                          24.7%; Score 450; DB 2; Le
33.3%; Pred. No. 1.7e-24;
ive 64; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.6%; Score 448; DB 2;
llarity 33.0%; Pred. No. 2.4e-24;
Conservative 59; Mismatches 136;
                                                                                                                                                                              Best Local Similarity .... Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local Simi
Matches 110;
                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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phosphotanstase system enzyme ii (EC 2.7.1.09) phosphoenotpyidvace-dependent, tren C; Species: Bacillus subtilis
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C; Accession: C69725; S67929; JC5037; I 40497; S67864
E; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmarson, P.T.; Entlan, K.D.; Errington, J.; Pabret, C.; Ferrari, Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A.; Authors: Foulger, D.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwa, A.; Oudega, B.; Park, S.H.; Parro, V.; Dohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Bosse, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Eagkeuchi, M.; Tamakoshi, A.; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Reference number: 14.0 < RUND  
A; Residues: 1-470 < RUND  
A; Crossion: 267929  
A; Crossion: 267929  
A; Experimental source: strain 168  
B; Helfert, C.; Gotsche, S.; Dahl, M.K.  
Mol. Microbiol. 16, 111-120, 1995  
A; Title: Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed by a phosp A; Reference number: 140497; MUID:95379486  
A; Reference number: 140497; MUID:95379486  
A; Reference number: 140497; MUID:95379486  
A; Reference number: 140497; MUID:95379486  
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A; Reference number: 140497; MUID:95379486  
A; Reference number: 140497; MUID:95479486  
A; Reference number: 140497; MUID:95479486  
A; Reference number: 140497; MUID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphotransferase system enzyme II (EC 2.7.1.69) phosphoenolpyruvate-dependent, treh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-139,'S',141-362,'L',364-464,'G',466-470 <SC2>
A; Cross-references: EMBL:254245; NID:g1000450; PIDN:CAA91014.1; PID:g1000451
C; Comment: This enzyme functions as the specific trehalose transporter. It belongs
C; Genetics:
                                                                                                                                                                                                                                                        KSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVAL 125
                                                                                                                                                                                                  7 VGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Gene: 1229; treB
C; Superfamily: phosphotransferase system sucrose-specific of Superfamily: phosphotransferase; sugar transport system C; Reywords: phosphotransferase; sugar transport system F;113-113/Domain: transmembrane #status predicted <PML>F;160-181/Domain: transmembrane #status predicted <PML>F;184-203/Domain: transmembrane #status predicted <PML>F;263-245/Domain: transmembrane #status predicted <PML>F;305-325/Domain: transmembrane #status predicted <PML>F;305-325/Domain: transmembrane #status predicted <PML>F;305-325/Domain: transmembrane #status predicted <PML>F;402-421/Domain: transmembrane #status predicted <PML>F;403-421/Domain: transmembrane #statu
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                                                Pred. No. 1.4e-17;
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A; Residues: 324-362, L',364-464,'G',466-470 <HEL>
A; Cross-references: EMBL:X80203; NID:9580941
R; Schoeck, F.; Dahl, M.K.
Gene 175, 59-63, 1996
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 GAAGFLGVVSIDAPDMVMFLVCAVVTFFI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.38; Pic.
                                                                                      Conservative
                                           Best Local Similarity
Matches 69; Conserv
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N.Alternate names: enzyme II-sucrose protein
S.Specias Vibrio alginolyticus
C.Specias Vibrio alginolyticus
C.Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 18-Jun-1999
C.Accession: JQ0781
R.Blatch, G.L.; Scholle, R.R.; Woods, D.R.
R.Blatch, G.L.; Scholle, R.R.; Woods, D.R.
A.Pitle: Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose uptake-ence A.Reference number: JQ0781
A.Accession: JQ0781
A.Accession: JQ0781
A.Accession: JQ0781
A.Residues: 1-479 <BLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05935.1; GSPDB:GNOC
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M76768; GB:M30194; NID:q155261; PIDN:AAA27555.1; PID:q155262
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C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor
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                                     1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQGA
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C;Superfamily: phosphotransferase system sucrose-specific enzyme II,
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1 Similarity 49.7%; Pred. No. 6.2e-22;
84; Conservative 32; Mismatches 47;
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Query Match

Search completed: March 21, 2002, 16:23:47 Job time: 153 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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12.6 280 7 US-10-072-851-12479 Sequence 12479, A 12.4 842 1 PCT USO2-03987-11950 Sequence 11950, A 12.4 842 1 PCT USO2-03987-11950 Sequence 11950, A 12.4 842 7 US-10-072-851-11950 Sequence 11950, A 12.2 263 1 PCT-USO2-03987-13018 Sequence 13152, A 12.2 263 6 US-09-815-242-13018 Sequence 13152, A 12.2 263 6 US-09-815-242-13152 Sequence 13152, A 12.2 263 7 US-10-072-851-13018 Sequence 13152, A 12.2 263 7 US-10-072-851-13018 Sequence 13152, A 12.2 263 7 US-10-072-851-13152 Sequence 13152, A 12.1 135 1 PCT-USO2-03987-5842 Sequence 5842, Ap 12.1 135 7 US-10-072-851-1309 Sequence 10809, A 12.1 135 7 US-10-072-851-1309 Sequence 10809, A 12.1 135 7 US-10-072-851-1309 Sequence 10809, A 12.1 142 1 PCT-USO2-03987-518 Sequence 5718, Ap 11.1 142 1 PCT-USO2-03987-5718 Sequence 5718, Ap 11.1 142 7 US-10-072-851-5718 Sequence 5718, Ap 11.1 142 7 US-10-072-851-5718 Sequence 5718, Ap 11.1 142 7 US-10-072-851-5718 Sequence 12272, Ap 11.1 142 7 US-10-072-851-5718	ALIGNMENTS  SULT 1 T-GS02-03987-13467 Sequence 13467, Application PC/TUS0203987 Sequence 13467, Application PC/TUS0203987 Sequence 13467, Application PC/TUS0203987 APPLICANT: Elitra Pharmaceuticals, Inc. TITLE OF INVENTION: Methods for Identifying the Target of a Compound which FILE REFERENCE: ELITRA.028VPC CURRENT APPLICATION NUMBER: PC12/020-02-02 CURRENT APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09 PRIOR FILING DATE: 2001-02-09 RIUMBER OF SEQ ID NOS: 15811 SOFTWARE: FastEQ for Windows Version 4.0 SEQ ID NO 13467 TYPE: PRT ORGANISM: Streptococcus pneumoniae TYPE: PRT ORGANISM: Streptococcus pneumoniae	aps 61	FGLGGFLIGGVHQLIVVSGVHHIFNLLEVQLLAADHANPFNAIITAAMTAQGAATVAV 345 FFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIK 121  :          : :	AVALGAAGFLG-VVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA 180            : :   :     :     :
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240 QLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEV
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517 VVYALADAEVSIAFPTGHAFGLKTR----NGAEVLIHVGIDTVSMNGDGFEAKVAQGNKV

300 KAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV

572

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us-09-604-231-4.rapn

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29.8%; Score 542; DB 7; Length 62 ilarity 36.0%; Pred. No. 1.3e-32; Conservative 74; Mismatches 130; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13467
LENGTH: 627
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Application US/10072851
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                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
Jiang, Bo
Boone, Charles
                                                                                                        Foulkes, J. Gordon
Zamudio, Carlos
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                                                     APPLICANT: Carr, Grant J. APPLICANT: Xu, H. Howard
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Best Local Similarity
Matches 128; Conservat
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Vammonto, Robert T.
APPLICANT: Yammonto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Incharyotes
FILE REFERENCE: ELITRA J1A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-10-33
PRIOR APPLICATION NUMBER: 60/25,565
PRIOR APPLICATION NUMBER: 60/25,565
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,7931
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
                                                                                                Sequence 13467, Application US/09815242 GENERAL INFORMATION:
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                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Matches 128; Conserv
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US-10-072-851-13467
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APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA, 0.28A
CURRENT APPLICATION NUMBER: US/10/07, 851
PRIOR APPLICATION NUMBER: 60/267, 636
PRIOR APPLICATION NUMBER: 60/267, 636
PRIOR PILING DATE: 2001-02-09
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TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA, 028 VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILIG DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 FGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAACLAV 61
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
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386 LVYAVIYYFVFRFLIVKLKYKTPGREDKQSQAVTASATELPYAVLEAMGGKANIKHLDAC 445
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566 SQGEVRAPFNGKVQMIFPTKHAIGL----VSDSGLELLIHIGLDTVKLNGEGFTLHVEEG
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;; Pred. No. 2.6e-15;
54; Mismatches 149;
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    PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
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CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                   ; ORGANISM: Staphylococcus aureus
US-09-815-242-5658
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Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
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24.6%;
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Best Local Similarity 24.69
Matches 111; Conservative
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US-10-072-851-5658
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         -----AFGAAIAYGLY------ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 ITRLRVEVNDKSKVDVPGLKDLGASGVLEVGNNMQAIFGPKSDQIKHEMQQIMNGQVVEN 505
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                                                                                                                                                                                                                                                                                    ----PPIELELFNQG---
                                                                                                                                                                                                                                              Indels 137;
                                                                                                                                                                                                 Length 679;
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu H. Howard.
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                           54; Mismatches 149;
                                                                                                                                                                                                 17.1%; Score 310.5; DB 1
24.6%; Pred. No. 2.6e-15;
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
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                                                                                                                                                                                                                                                                                    7 VGGLLFGLVYSPIVITGLHQSF----
                                                                                                              ; ORGANISM: Staphylococcus aureus PCT-US02-03987-5658
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Best Local Similarity
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APPLICANT:
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211 VAVFLEGFIKRLLIPFGLHHIFHAPFWFEFGSWKNAAGEIIHGDQRIFIEQIREGAHLTA 270
                                                                                                                    177 ATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP 236
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                                                                                                                                                                                                                             331 VAPLLFFI---HAVLDGLSFLTLYLLDVHLGYTFSGGFIDYVLLGVLPNKTQWWLVIPVG 387
                                                                                                                                                                                                                                                                             448 ITRLRVEVNDKSKVDVPGLKDLGASGVLEVGNNMQAIFGPKSDQIKHEMQQIMNGQVVEN 507
                                                                                        40 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSA----VLGITEPAIFGVNL 95
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
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SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12270
  7 VGGLLFGLVYSPIVITGLHQSF-
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LENGTH: 681
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GENERAL INFORMATION:
APPLICART: Elitra Pharmaceuticals, Inc.
APPLICART: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5658
LENGTH: 679
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: 60/267,636
                                                                                                                                                        ; ORGANISM: Staphylococcus aureus US-10-072-851-5658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Staphylococcus aureus
PCT-US02-03987-12270
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Matches 111; Conservative
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Best Local Similarity 24.69
Matches 111; Conservative
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LENGTH: 681
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Sequence 10089, Application PC/TUS0203987

GENERAL INFORMATION:
APPLICAMT: Biltra Pharmaceuticals, Inc.
APPLICAMT: Biltra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.0280PC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR FILING DATE: 2001-02-09
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                                                         290 LLYLLHALLTGISLFVATLLGIHAGFSFSAGAIDYALMYNLPAASQNVWMLLVMGVIFFA 349
                                                                                                                            ----RNGSIDPD 176
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   Gaps
                                    ----- PPIELELFNQG---- 39
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                                                                                                        GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSA----VLGITEPAIFGVNL
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 Indels 137;
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 149;
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23.2%; Pred. No. 3.5e-14;
Live 62; Mismatches 162;
   Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10089
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 54;
                                     VGGLLFGLVYSPIVITGLHQSF --
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PCT-USO2-03987-10089
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Best Local Similarity
Matches 114; Conserv
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   Matches 111;
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                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PITMEDDKDETVVVAEDKSATSELSHIVHAPLTGEVTPLSEVPDQVFSEKMMGDGIAIKP 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGEVRAPFNGKVQMIFPTKHAIGL----VSDSGLELLIHIGLDTVKLNGEGFTLHVEEG 623
                                                                                            331 VAPLLFFI---HAVLDGLSFLTLYLLDVHLGYTFSGGFIDYVLLGVLGVKTQWWLVIPVG 387
                                                                                                                                                                                                                                                                                                                   447
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                                                                        -PPIELELFNQG---- 39
                                                                                                                                         40 GSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGASGVSA----VLGITEPAIFGVNL
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 Length 681;
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; Score 310.5; DB 6;
; Pred. No. 2.6e-15;
54; Mismatches 149;
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Pred. No. 2.6e-15;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12270, Application US/10072851
GENERAL INFORMATION:
                                                                    7 VGGLLFGLVYSPIVITGLHQSF-----
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APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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 17.1%;
24.6%;
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24.6%;
                                    Matches 111; Conservative
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Boone, Charles
                   Similarity
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Best Local Similarity
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 Query Match
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DD 230 MSGFFPIMMFGLPGAALAMYFAAPKERRPMVGGMLLSVAVTAFLTGVTEPLEFLFMFLAP	Oy 92GVNLRLRWPFFIGIGTAAIGGAL	Qy 115VALGAA  Qy 115VALGAA    :  :  Db 350 IYFVVFSLVIRMFNLKTPGREDKEDEIVTEEANSNTEEGLTQLATNYIAAVGGTDNLKAI	QY 129	Qy 164 LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF :	Qy 224 ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN	QY 284 LNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI  DD 577 LEGKGFKRLVEEGAQVSAGQPILEMDLDYLNANARSMISPVVCSNIDDFSGLIIKAQGHI	Qy 344 EAGANLLNVAKK 355  Qy 344 EAGANLLNVAKK 355  Db 637 VAGQTPLYEIKK 648	RESULT 12 US-10-072-851-10089 : Sequence 10089, Application US/10072851	GENERAL INFORMATION:  APPLICANT: Carr, Grant J.  APPLICANT: Xu, H. Howard	; APPLICANT: Foulkes, J. Gordon ; APPLICANT: Zamudio, Carlos ; APPLICANT: Haselbeck, Robert	; APPLICANT: Ohlsen, Kari L. ; APPLICANT: Zyskind, Judith W. ; APPLICANT: Wall, Daniel	/ APPLICANT: Trawick, John D. / APPLICANT: Yamamoto, Robert T. / APPLICANT: Roemer, Terry	-	; TITLE OF INVENTION: Methods for identifying the Target of a Compound ; TITLE OF INVENTION: Proliferation ; FILE REFERENCE: ELITRA.028A	; CURRENT APPLICATION NUMBER: US/10/072,851 ; CURRENT FILING DATE: 2002-02-08 ; DPIOD APPLICATION NUMBER: 6/257 536	PRIOR FILLIG DATE: 2001-02-09  NUMBER OF SEQ ID NOS: 15811	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 10089 ; LENGTH: 648	; TIPE: PAI ; ORGANISM: Bscherichia coli US-10-072-851-10089		Hest Local Similarity 23.24; Fred. No. 3.96-14; Matches 114; Conservative 62; Mismatches 162;	Qy 5 GPVGGLLFGLVYSPIVITGLHQSFPPI
:    :    :	QY 129GPLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163 Db 410 DACITRLRLTVADSARVNDTMCKRLGASGVVKLNKQTIQVIVGAKAESIGDAMKKVVARG 469	QY 164 LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF 223  1	QY 224 ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 283	QY 284 LNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 343 	Qy 344 EAGANLLNVAKK 355 	RESULT 11 US-09-815-242-10089 : Sequence 10089, Application US/09815242	) (E, E,	; APPLICANT: Wall, Daniel ; APPLICANT: Trawick, John D. ; APPLICANT: Carr, Grant J. ; APPLICANT: Xamamoto, Robert T.	; APPLICANT: Xw, H. Howard ; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokarvotes	NCE: ELIT LICATION ING DATE:	; PRIOR APPLICATION NUMBER: 60/191,078 ; PRLOR FILING DATE: 2000-03-21 ; PRLOR APPLICATION NUMBER: 60/206,848	FRION FILING DATE: 2000-05-23 FRIOR APPLICATION NUMBER: 60/207,727 FRIOR FILING DATE: 2000-05-26	; PRIOR APPLICATION NUMBER: 60/242,578 ; PRIOR PELICATION UNMBER: 60/253,625	; FRLOR APPLICATION UNMBER: 60/257,931 ; PRIOR APPLICATION UNMBER: 60/257,931 ; PRIOR FILING DATE: 2000-12-22	PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16 NIMMER OF SEC ID NOS: 14110	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 10089	; LENGTH; 648 ; TYPE: PRT ; OKGANISM: Escherichia coli	2 COUNT 242 CTO CO	West Local Similarity 13.2%; Pred. No. 3.5e-14; Matches 114; Conservative 62; Mismatches 162; Indels 154; Gaps 12;	5 GPVGGLLFGLVYSPIVITGLHQSFPPI*ELELFNQGGSF	Db 170 GALGSGIFGFINRLLIPTGLHOVLNTIAMFQIGEFTNAAGTVFHGDINRFYAGDGTAGMF 229

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CURRENT APPLICATION NUMBER: PCT/US02/03987 CURRENT APPLICATION NUMBER: PCT/US02/03987 CURRENT FILING DATE: 2002-02.
PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FASTERO for Windows Version 4.0
                                                                                            ; Sequence 10500, Application PC/TUS0203987; GENERAL INFORMATION:
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US-09-815-242-10500
; Sequence 10500, Application US/09815242
; GENERAL INFORMATION:
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PCT-US02-03987-10500
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T
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Zyskind, Judith W.
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Matches 107; Conservative
                                                             RESULT 14
PCT-US02-03987-10500
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LENGTH: 551
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GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
APPLICANT: Huesing, Joseph E.
APPLICANT: Huesing, Joseph E.
APPLICANT: Hasing, Joseph E.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION Xenrical Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR PILING DATE: 2000-06-30
                                                                                                                                                                                                                                  410 DACITRLRLTVADSARVNDTMCKRLGASGVVKLNKQTIQVIVGAKAESIGDAMKKVVARG 469
                                                                                                                                                                                                                                                                                                ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 283
                                                                                                                                                                                                                                                                                                                                                              ----GFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYG 163
                                                                                                                                                                                                                                                                            LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF 223
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                                                                                                                                                                           350 IYFVVFSLVIRMFNLKTPGREDKEDEIVTEEANSNTEEGLTQLATNYIAAVGGTDNLKAI 409
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                                                                                                          290 LLYLLHALLTGISLFVATLLGIHAGFSFSAGAIDYALMYNLPAASQNVWMLLVMGVIFFA
                                                                                                                                              ------VALGAA-----
             43 IFATASMANIAQGAACLAVFFLAKSEK---LKGLAGASGVSAVL-GITEPAIF----
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CRCANISM: Xenorhabdus sp.
US-09-897-516-6783
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Matches 54; Conserv
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US-09-897-516-6783
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APPLICANT: Elitra Pharmaceuticals, Inc. TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibit TITLE OF INVENTION: Proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 ----FATASMANIAQGAACLAVFFLAKSEKLKGLAG---ASGVSAVL-GITEPAIFGVNL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 NLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.2%; Score ... 6.8e-1., 23.0%; Pred. No. 6.8e-1., ... 68; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 PMMLVVQGLVFAAIYYFGFRFAITKFNLMTPGREEGDGEETPDVAEGDNKFASLARRIYD 303
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304 GLGADANVTSIDNCTTRLRLTVKDTGKVDQAKIKATGVPGVKVIDDTNIQVIVGTEVQFV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 ------DATAAPV---PAGTIKAEAEAPAEFSNDSTIIQAPLIGEAIALSSVSDAM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 ADEMORLYNHQAPATPVKETPVSQPVVEKKAPV--STKETELYSVANGKVIPISEVPDDV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 FASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 ----FATASMANIAQGAACLAVFFLAKSEKLKGLAG---ASGVSAVL-GITEPAIFGVNL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 551;
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 NLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GPVGGLLFGLVXSPIVITGLHQSFPPI---ELELFNQGGSFI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.2%; Score 276.5; DB 6; 23.0%; Pred. No. 6.8e-13; iive 68; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LVRRNGSIDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Enterococcus faecalis
US-09-815-242-10500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 ----MVMFLVCAVVTFF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 15.2%
Best Local Similarity 23.0%
Matches 107; Conservative
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Search completed: March 21, 2002, 16:27:37 Job time: 338 sec

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Sequence 3 Sequence 8 Sequence 8 Sequence 1 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 5 Sequence 2 Sequence 3 
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Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PAYNE, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: MOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK CLONE: -811A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/828,788A FILING DATE: 19920129 CLASSIFICATION: 435 ATTORNEY/AGENT INPORMATION: NAME: SALIWANCHIK, DAVID R. REFERENCE/DOCKET NUMBER: 31,794 REFERENCE/DOCKET NUMBER: MA75 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: 904-375-8100 TELEFEAX: 904-372-5800
           US-08-622-740-8
US-08-640-689-8
US-09-042-426-110
US-09-330-760-110
US-09-330-760-110
US-09-330-760-110
US-09-330-7737-110
US-09-330-473-110
US-07-671-817A-5
US-07-671-817A-5
US-08-349-867-13
US-08-249-867-13
US-08-239-476-19
US-08-239-476-19
US-08-239-476-19
US-08-239-476-19
US-08-46-486-2
US-08-639-308-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/07828788A Patent No. 5273746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
2439
614
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11155
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID R. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: AMINO ACID
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-07-828-788A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
 STATE:
 Sequence 1, Appli
Patent No. 5164180
Patent No. 5188950
Sequence 3, Appli
Sequence 35, Appl
Patent No. 5254799
Sequence 7, Appli
Patent No. 5523211
Sequence 7, Appli
Sequence 7, Appli
                                                                                                                                               (without alignments)
377.488 Million cell updates/sec
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Sequence 2, Appli
Sequence 12, Appl
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Sequence 2, Al
Sequence 6, Al
Sequence 10,
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Sequence
Sequence
                                                                                                                             ; Search time 21.58 Seconds
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-463-308-7
US-08-836-325-2
US-08-446-486-6
US-08-157-363A-10
US-08-463-308-6
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US-08-933-891-2
PCT-US92-11337-12
US-08-040-751-1
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PCT-US93-11405-10
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US-08-836-325-12
US-08-674-351-2
US-08-836-325-15
US-09-413-814-70
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US-08-894-818B-35
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US-08-810-720-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
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                                                                                                                             March 21, 2002, 16:23:16
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
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Match
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Result No.

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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                            US-08-356-034-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5691308el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 5691308el Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                             13;
                                                                                                                 377 LEVLDGTEFSFASLTADLPSTIY--RQRGTVDSLDVIPPQDNSVPARAGFSHRLSHVTML 434
                                                                                                                                                                                          231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                                                                                                                                                                                                                                         494 DILKITSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS 548
                                                                                                                                                                                                                                                                                                                                 291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                         549 ATMSSGGULQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 593
                                                                                 143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-----TTK 188
                                             Gaps
                                                                                                                                                                189 AEA-----EAP-----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS
  Length 1176;
                                             Indels
6.2%; Score 113.5; DB 1; 22.4%; Pred. No. 0.0076; tive 43; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/356,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21,023
REFERENCE/DOCKET NUMBER: MA43.C1.D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/210,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/865,168
FILING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08356034
Patent No. 5691308
GENERAL INFORMATION:
GAPLICANT: Payne, Jewel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Saliwanchik, Roman REGISTRATION NUMBER: 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                          Conservative
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594 YIERIEFVPA 603
                                                                                                                                                                                                                                                                                                                                                                                                               351 NVAKKEAVPA 360
Query Match
Best Local Similarity
Matches 56; Conserv
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COUNTRY:
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Sequence 2, Application US/08933891
Patent No. 6096708
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 6096708e1 Bacillus thuringiensis Isolate
TITLE OF INVENTION: Active Against Lepidopteran Pests, and Genes Encoding
TITLE OF INVENTION: No. 6096708e1 Lepidopteran-Active Toxins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 DILRITSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS 548
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                                                                                                                                                                                                                                                                                                                          STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 113.5; DB 1;
22.4%; Pred. No. 0.0076;
tive 43; Mismatches 96;
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PatentIn Release #1.0, Version #1.25
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                      ORGANISM: BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/933,891 FILING DATE:
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TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 22.4%
Matches 56; Conservative
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CURRENT APPLICATION DATA:
                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
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594 YIERIEFVPA 603
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STAAL.

COUNTRY: USA
ZOUNTRY: USA
ZOUNTRY: USA
ZOUNTRY: 2266
ZDP: 32666
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
COMPUTERY APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337
S: DAVID R. SALIWANCHIK
2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                     FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-372-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12:
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Best Local Similarity 22.4%;
Matches 56; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                STREET: 2421 N.W. CITY: GAINESVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
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ORIGINAL SOURCE:
 ADDRESSEE:
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GENERAL INFORMATION:
APPLICANT: PAYUR, JEWEL M.
APPLICANT: HICKLE, LESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK ; CLONE: 811A2 US-08-933-891-2
                                                            APPLICATION NUMBER: 07/865,168
FILING DATE: 09-APR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/451,261
FILING DATE: 14-DEC-89
FILING DATE: 17-DIN-89
ROPLICATION NUMBER: 07/371,955
FILING DATE: 27-JUN-89
ATTORNEY/AGENT INFORMATION:
NAME: SAILWANCHIK, ROMBN
REGISTRATION NUMBER: 21,023
REFERENCE/DOCKET NUMBER: DA33.C1.D1
US/08/356,034
                                 US/08/210,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: BACILLUS THURINGIENSIS
STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                   TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID No: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 1176 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANGE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER:
                               APPLICATION NUMBER:
                                                FILING DATE:
APPLICATION NUMBER:
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594 YIERIEFVPA 603
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HYPOTHETICAL: Y
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189 AEA-----EAP----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 230
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                                                                                                                                                                                                    Gaps
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                                                                                                                                                     Length 1176;
                                                                                                                                                  6.2%; Score 113.5; DB 5; Length 2.4%; Pred. No. 0.0076; ve 43; Mismatches 96; Indels
                                                                                                                                                                                                                                                   143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
CLONE: 811A2
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US-08-040-751-1
'Sequence 1, Application US/08040751
'Patent No. 5407825
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143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG-----TTK 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 LFVLDGTEFSFASLTADLPSTIY--RQRGTVDSLDVIPPQDNSVPARAGFSHRLSHVTML 437
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                      Length 1129;
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                                                   ;Patent No. 5164180
; APPLICANT: Payne, Jewel;Sick, August J.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS ISOLATES ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Patent No. 5188960
; APPLICANT: PAYNE, JEWEL; SICK, AUGUST J.
ITILE OF INVENTION: BACILLUS THURINGIENSIS ISOLATE ACTIVE
; AGAINST LEPIDOPTERAN PESTS, AND GENES ENCODING NOVEL
; LEPIDOPTERAN-ACTIVE TOXINS
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; Pred. No. 0.039;
42; Mismatches 97;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/451,261
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 371,955
; SEQ ID NO:2:
                                                                                                                                                             APPLICATION NUMBER: US/07/451,389
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 353,860
FILING DATE: 18-MAY-1989
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                                                                                                                                                                                                                                                                                                                                                        5.8%;
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Best Local Similarity 22.4%;
Matches 56; Conservative 4
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Best Local Similarity 22.4%
Matches 56; Conservative
                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                           AGAINST LEPIDOPTERAN PESTS (
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597 YIDRIEFVPA 606
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5188960-2
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5188960-2
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             APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5407825el Bacillus thuringiensis isolates
TITLE OF INVENTION: active against Lepidopteran Pests and Genes Encoding No. 54078
TITLE OF INVENTION: Lepidopteran-active Toxins
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 AEA-----EAP----AEFSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TTK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 DILRITSPGQISTL---RVTITAPLSQRYRVRIRY--ASTTNLQFHTSIDGRPINQGNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 MFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 113.3,
Pred. No. 0.0076;
                                                                                                                                                ADDRESSEE: DAVID R. SALIWANCHIK
STREET: 2421 N.W. 41st STREET, SUITE A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%; Score 113.5; 22.4%; Pred. No. 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORREY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVID R.
REFERENCE/DOCKET UNMBER: MA39.C1.D3
TELECHONE: 904-375-8100
TELEPHONE: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/040,751
FILING DATE: 19930329
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: AIZAWAI
INDIVIDUAL ISOLATE: PS811
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 ATMSSGGNLQSG----
                                                                                                                                                                                  GAINESVILLE
                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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597 YIERIEFVPA 606
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Matches 56; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                               STREET:
CITY: GA
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1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL----FNQGGSFIFAT----ASMAN 51
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                                                                                                                52 IAQGAACLAVFFLAKSEKLKGLA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TATELECOMMUNICATION INFORMATION: TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: TAKAKURA, Hikaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2C CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 MHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20004
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US-08-894-818B-35
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                                                                                                                                                               552 ATMSSGGNLQSG-----SFRTAGF--TTPF---NFSNGSSIFTLSAHVFNSG-NEV 596
438 SQAAGAVYTLRAPTFSWRHRSAEFSNLIPSSQITQIPLT-KSINLGSGTSVVKGPGFTGG 496
                                          231 GVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFN 290
                                                                             497 DILRRTSPGQISTL---RVIITAPLSQRXRVRIRY--ASTINLQFHTSIDGRPINQGNFS 551
                                                                                                                                   291 PLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= Xaa at position 428 is Gly or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HYPERTHERMOSTABLE PROFEASE GENES NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAKAKURA-1
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APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/894,818B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C.
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08894818B Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORISHITA, Mio
YAMAMOTO, Katsuhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TAI TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MITTA, Masanori
APPLICANT: ASDA, Kiyozo
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                            351 NVAKKEAVPA 360
                                                                                                                                                                                                                                                                      597 YIDRIEFVPA 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20004
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                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-894-818B-3
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---VNLRLRWPFFIGI-----GTAAIGGALIALFNIKAVALGAAGFLG--------- 132
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                                                                                                                                                                                                                                                                                                                                                                                       PDATAAP-----VP--AGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGSGVAI------VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDIL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 VNAYKAINYDNYAKLVFTGYVANKGS----QTHQFVI---SGASFVTATLYWDNANSDLD 349
------GASGVSAVLGITEPAI-----FG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MORISHITA, MIO
APPLICANT: YANAMOTO, KAISUNIKO
APPLICANT: ARADA, MASANOri
APPLICANT: ASADA, KIYOZO
APPLICANT: TSUNASAWA, SUSUMU
APPLICANT: TSUNASAWA, SUSUMU
APPLICANT: KATO, IKUNOSALI
TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GFDTVNLNGTHFNP 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 LYLYDPNGNQVDYSYTAYYGFEKVG----YYNP 378
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APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-00v-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C. COUNTRY: United States of America
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382 -GPNNQEFSVLDGTEF--SFASLTINPSTIYRQRGTVDSLDVEIPPQDNSVPPRAGFSHR 438
  SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVSI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              543 FHISIDGRPINQGNFSATMSSGSNLQSG------SFRIVGF--TTPF---NFSNGSS 588
                                                                                                                                                                                                                      --TTKAEAEAPAEFSN---DSTIIQAPLTGEAIALSSVSDAMFA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNIKAVALGAAGFLGVVSI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 -GPNNOEFSVLDGTEF--SFASLTINPSTIYRORGIVDSLDVEIPPQDNSVPPRAGFSHR 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 MHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TTKAEAEAPAEFSN---DSTIIQAPLTGEAIALSSVSDAMFA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSHVTMLSQAAGAVYTLRATFSWQHRSAEFNNIIPSSQITQIPLT-------K 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 SPIVITGLHQSFPPIELELFNQGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5254799

Marcar: DeGreve, Henri M. J.; Salgado, Maria B.L.; Van
Montagu, Marc C.E.; Vaeck, Mark
Jan J.A.; Hofte, Hermanus F.
Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.; Jan J.A.;
                                                                                                                                                                                                                                                                                                                                                                  137 DAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----PDATAAPVPAG----
                                                                                                                                                                                                                                                                                                                                  SGKLGSGVAIVP----TKGQLVSPVSG-----KIVVAFPSGHAFAVRTKAEDGSNVDIL
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                                                         --RRIILGS-----
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                                                      ----PVLSLTGLGIFRT---LSSPLY---
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5254799-7
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5254799-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 --VVSIDAPDMVMFLVCAVVTFFIAFG------AAIAYGLYLV--RRNGS----ID 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDATAAP-----VP--AGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGSGVAI-------VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDIL 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 IAQGAACLAVFFLAKSEKLKGLA-----FG 92
                                                                                                                                                                                                                                                                                                                                                                                   1 YDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL----FNQGGSFIFAT----ASMAN 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 SPIVITGLHQSFPPIELELFNQGGSFIFATASMANIAQGAACLAVFFLAKSEKLKGLAGA 76
                                                                                                                                                                                                                                                                      ; Score 99.5; DB 4; Length 654;
; Pred. No. 0.089;
63; Mismatches 114; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DeGreve, Henri M. J.; Salgado, María B.L.; Van, Montagu, Marc C.E.; Vaeck, Mark A.; Zabeau, Maarcus F. O.; Leemans, Jan J.A.; Hofte, Hermanus F. P. F. TITLE OF INVENTION: TRANSFORMATION VECTORS ALLOWING EXPRESSION: OF BACILLUS THURINGIENSIS ENDOTOXINS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 1184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.4%; Score 98; DB 6
19.9%; Pred. No. 0.33;
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482 LYLYDPNGNQVDYSYTAYYGFEKVG----YYNP 510
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/555,828
FILING DATE: 23-UUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 821,582
FILING DATE: 22-JAN-1986
APPLICATION NUMBER: 692,759
FILING DATE: 18-JAN-1985
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                                                                                                                                                                                                                                                                 5.5%;
                      SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             81; Conservative
                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPDLOGY: linear
MOLECULE TYPE: peptide
INFORMATION FOR SEQ ID NO:
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Best Local Similarity
Matches 77; Conserv
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;Patent No. 5254799
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5254799-6
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  1697 FETFGNSMICLFQITTSA-GWDGLLAPILNSGPPDCDPEKDHPGSSVKGDCGNPSVGIFF 1755
                                                                                                                                                                                      1811 ------QFIEFCKLSD--FAAALDPPLLIAKPNKVQLIAMDLPMVSGDRIHCLDILFAF 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 ISTLRVNITAPLSQRYRVRIRY -- ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSG- 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 LVRRNGSID-----PDATAAPVPAG-----TTKAEA-----EAP-----AE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 IYRQRGTVDSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAPTFSWQHRSAE 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 FSN---DSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVP----TKGQLVSPVSG-- 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 ----KIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE 303
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                                                144 FLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTI
                                                                                                                                          204 IQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVS----PVSGKIVVAFPSGHAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: IDENTIFICATION, QUANTITATION AND PURIFICATION OF INSECTICIDAL PROTEINS FROM BACILLUS THURINGIENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSECTICIDAL COTTON PLANTS (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PUSZTAI-CAREY, MARIANNE; CAREY, PAUL R.; LESSARD,
                                                                                                                                                                                                                                                              260 AVRTKAEDG--SNVDILMHIGFDTVNLNGTHFNP----LKKQGDEVKA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.3%; Score 96.5;
22.4%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,076
FILING DATE: 19-7UL-1994
PRIOR APPLICATION NUMBER: 102,491
FILING DATE: 19-F88-1992
APPLICATION NUMBER: 836,967
FILING DATE: 19-F88-1992
APPLICATION NUMBER: 493,453
FILING DATE: 14-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 13, Application US/08810720; Patent No. 6037527; GENERAL INFORMATION:

APPLICANT: Barton, Kenneth A. APPLICANT: Umbeck, Paul F. TITLE OF INVENTION: INSECTICIDAL CONRESPONDENCES. 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nicholas J. Seay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Nicholas J. Seay
One South Pinckney Street
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Best Local Similarity
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;Patent No.
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                                                                                                                                                                                                                                                                        APPLICANT: Mandel, Gail
APPLICANT: Malegoua, Simon
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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543 FHTSIDGRPINQGNFSATMSSGSNLQSG-----SFRTVGF--TTPF---NFSNGSS 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --MVM 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C 1100 New York Ave., N. W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 LKGLAGASGVSAV---LGITEPAIFGVNLRLRWPFFI----GIGTAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ---IGGALIALFNIKAVALGAAGFLG-VVSIDAPD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
RECOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                           335 VNTYGLGEIEAGANLLNVAKKEAVPA 360
                                                                           Sequence 7, Application US/08836325
Patent No. 6110672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 22.2
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-836-325-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: DC
STATE: DC
COUNTRY: USA
TO: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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STREET: 11
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completed: March 21, 2002, 16:23:18
he: 149 sec
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Matches
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Job time:
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APPLICANT: Leemans, Jan Jozef A
APPLICANT: Leemans, Jan Jozef A
APPLICANT: Hofte, Hermanus Fransiscus P
TITLE OF INVENTION: TRANSFORMATION VECTORS ALLOWING
TITLE OF INVENTION: EXPRESSION OF FOREIGN POLYPEPTIDE ENDOTOXINS FROM BACILLUS
TITLE OF INVENTION: THURINGIENSIS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 FNNIIPSSQITQIPLT------KSTNLGSGTSVVKGPGFTGGDILRRTSPGQ 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         507 ISTLRVNITAPLSQRYRVRIRY -- ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 LLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.3%; Score 96.5; DB 3; Length 648; Best Local Similarity 22.4%; Pred. No. 0.18; Matches 53; Conservative 33; Mismatches 78; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Burns, Doane, Swecker & Mathis
George Mason Bldg., Washington & Prince Sts
                                                                            OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,720
FILING DATE: 03-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 670513.90163
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
TELEPAX: 608/251-9166
INFORMATION POR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 LVRRNGSID-----PDATAAPVPAG-----TTKAEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       De Greve, Henri Marcel J
Salgado, Maria Benita Leonor
Van Montagu, Marc Charles E
Vaeck, Mark A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08446486
Patent No. 5545565
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                         648 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-810-720-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESSE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Salgado,
APPLICANT: Salgado,
APPLICANT: Van Mont
APPLICANT: Zabeau,
APPLICANT: Leemans,
APPLICANT: Leemans,
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
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COMPUTER READABLE FORM:

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166 LVRRNGSID-----PDATAAPVPAG-----TTKAEA-----EAP-----AE 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "deduced amino acid sequence
of B.t. sotto (Shibano et al., Gene 34, p. 243,
1985)"
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                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-JAN-1985
ATTORNEY/AGENT IRFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REPERENCE/DOCKET UMBER: 010830-047
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,965
FILING DATE: 08-0CT-1993
APPLICATION NUMBER: US 08/014,148
FILING DATE: 05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 06/821,582
FILING DATE: 22-JAN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/692,759
                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,486
FILING DATE:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/555,828 FILING DATE: 23-JUL-1990 PRIOR APPLICATION DATA:
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   934 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                FILING DATE: 08-OCT-1
APPLICATION NUMBER: U
FILING DATE: 05-FEB-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COCATION: 1.934
CTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
US-08-446-486-7
COMPUTER: IBM PC COPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
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nes 53; Conserv
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protein search, using sw model ı OM protein Run on:

March 21, 2002, 16:22:45 ; Search time 42.58 Seconds
 (without alignments)
 629.745 Million cell updates/sec

US-09-604-231-4 1821 1 YDFGGPVGGLLFGLVYSPIV.....IEAGANLLNVAKKEAVPATP 362 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

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/SIDSB/gcgdata/geneseg/genesegp/AA1994.DAT:\* /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDS8/gcgdata/geneseg/genesegp/AA1996.DAT:\*/SIDS8/gcgdata/geneseg/genesegp/AA1997.DAT:\*/SIDS8/gcgdata/geneseg/genesegp/AA1998.DAT:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	C.qlutamicum phosp	C.glutamicum phosp	C glutamicum prote	Brevibacterium lac	C qlutamicum prote	C.glutamicum phosp	Escherichia coli p	C.glutamicum phosp	B. burgdorferi ant	Amino acid sequenc	B. burgdorferi ant
SUMMARIES	ID		AAB66707	AAG92650	AAB69080	AAG93207	AAB66721	AAG98282	AAB66723	AAY20012	AAY53620	AAY20013
	æ	22	22	22	22	22	22	22	22	50	21	20
	% Query Match Length DB	362	468	661	661	683	683	648	135	167	583	135
	% Query Match	100.0	100.0	100.0	99.2	21.4	21.4	16.2	12.9	12.8	12.2	9.1
	Score	1821	1821	1821	1806	390.5	390.5	295	234	233.5	221.5	166.5
	Result No.	1	7	e	4	2	9	7	8	σ	10	11

Amino acid sequenc Human ORFX ORF555		C glutamicum prote	Delta endotoxin.	Human adult form o	Human neonatal for	Alteromonas lipase	Alteromonas lipase	B.thuringiensis to	Novel toxin expres	C glutamicum prote	Amino acid sequenc	T. halophilus xyul	C glutamicum prote	Peptide #1570 enco	Peptide #1628 enco	Peptide #1559 enco	Peptide #2757 enco	Human adult form o	Streptomyces globi	Streptomyces globi	P.denitrificans CO	C. glutamicum SRT	C glutamicum prote	Hyperthermostable	Pyrococcus furiosu	Hyperthermostable	Pyrococcus furiosu	Hyperthermostable	Rat multidrug resi	Rat multidrug resi	Enterococcus faeca	, Human adult form o
AAB40791	AAY81556	AAG90449	AAR39755	AAB99678	AAB99679	AAY21797	AAY21796	AAR08258	AAR25826	AAG91953	AAW59912	AAW58862	AAG90809	AAM15136	AAM27591	AAM02877	AAM04075	AAB99674	AAB13578	AAB13605	AAR13498	AAB78983	AAG92907	AAW94836	AAW24122	AAW94838	AAW24129	AAW94841	AAY70596	AAY70597	AAY00194	AAB99676
18	21	22	14	22	22	20	20	11	13	22	19	19	22	22	22	22	22	22	21	21	12	22	22	20	18	20	18	20	21	21	20	22
126	449	805	1176	1951	1951	908	809	1179	1179	404	1291	474	655	405	405	405	405	2009	521	521	459	697	772	412	522	522	654	654	1272	1272	440	2002
9.9	8.3			6.2		٠		5.8														5.5		5.5				5.5	5.4	5.4	5.4	5.4
161.5 154		118.5		112	112	108.5	108.5	106.5	106.5	105	105	102.5	102	101.5	101.5	101.5	0	101.5	101	101	100.5	100.5	100.5	6	6	99.5	9.	9.	66	66	98.5	
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## ALIGNMENTS

RESULT

Phosphoenolpyruvate; sugar phosphotransferase system; PTS. C.glutamicum phosphoenolpyruvate protein #2. AAB66708 standard; protein; 362 AA. 99US-0142691. 99US-0150310. 99DE-1042095. 99DE-1042097. 27-JUN-2000; 2000WO-IB00973. Corynebacterium glutamicum 09-APR-2001 (first entry) WO200102583-A2 23-AUG-1999; 03-SEP-1999; 03-SEP-1999; 01-JUL-1999; 11-JAN-2001. AAB66708; AAB66708 

Schroeder H, Zelder O, Haberhauer G; Pompejus M, Kroeger B, WPI; 2001-080989/09. (BADI ) BASF AG.

Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers

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Corynebacterium glutamicum
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                            Pompejus
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                                  The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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                                                                                                                                              100.0%; Score 1821; DB 22;
100.0%; Pred. No. 6.5e-171;
tive 0; Mismatches 0; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.glutamicum phosphoenolpyruvate protein #1.
                  Page 104-106; 144pp; English.
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99DE-1042095.
99DE-1042097.
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                                                                                                                                                                 Conservative
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for transformation
                                                                                                                                                        Similarity
                                                                                                                     362 AA;
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23-AUG-1999;
03-SEP-1999;
03-SEP-1999;
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Best Local S:
Matches 362
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                  Claim
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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  Haberhauer
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                                                                                          encoding
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  Zelder
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                                                                                                                                                                                                                 Claim 4; Page 101-102; 144pp; English.
  Schroeder H,
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  Kroeger
                                              WPI; 2001-080989/09
                                                                                                                                                                    for transformation
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI 120
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Pred. No. 1.6e-170;
Wismatches 0;
                                                                                                                                                                                                        H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                           18-DEC-2000; 2000EP-0127688.
                                                                                                          16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
                                                                                                                                          03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 362; Conservative
                                                                                                                                                                                                        Mizoguchi Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Patent Office
                                                                                                                                                                                                                                                        2001-376931/40.
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               EP1108790-A2
                                           20-JUN-2001
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Tateishi N
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                                                                                                    AGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA 360
                                                                                                                 PVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
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The present sequence represents the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity.
                                                                                                                          Brevibacterium lactofermentum sucrose PTS enżyme II protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzym
II obtained by cassette ligation-mediated amplification of downstream
domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFFIGIGTAAIGGALIALFNI 120
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Pred. No. 4.7e-169;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                           Kurahashi
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                                Ä
                               AAB69080 standard; Protein; 661
                                                                                                                                                                                                                    Brevibacterium lactofermentum
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                                                                                           (first entry)
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Matches 359;
                                                            AAB69080;
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RESULT
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307 ivipllypflyplglhwplnaimignintlgydfiggpmgawnfacfglytgyflls1ke 366
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                                                                                                                                                                                                                                                                                     LLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQGAACLAVFFLAKSE
                                                                                                                                                                                                                              427 fvftslltipamd--pwlgytigiavaffvsmflvlald---yrsneerdearakvaadk
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                                                                                                                                                                                                                                                                   -----PDAT-AAPV-----PAGTTKAEAEAPAEFSNDSTIIQAPLTGE
                                                                                                                                                                                               LGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphoenolpyruvate; sugar phosphotransferase system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.glutamicum phosphoenolpyruvate protein #5.
     Pred.
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| 558 fgeiegipadqanssttvikvngk 681
 Local Similarity 30.7%; Proces 118; Conservative 60;
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99US-0150310.
99DE-1042095.
99DE-1042097.
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23-AUG-1999;
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03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                    241 LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVK 300
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pvpagttkaeaeapaefsndstiiqapltgeaialssvsdamfasgklgsgvaivptkgg
                                                    Yokoi
                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid synthesis; vitamin; saccharide;
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da M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                         C glutamicum protein fragment SEQ ID NO: 6961.
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                                                                                                                                                                                                                                                                                                  AAG93207 standard; Protein; 683 AA.
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Senoh A, Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
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2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Coryneform bacterium;
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03-AUG-2000;
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Tateishi N,
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AAG93207;

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AAG93207 RESULT

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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the
ö
Haberhauer
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Schroeder H, Zelder
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Sequence

Query Match

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6
identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
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                                                                                                                                                            Gaps
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                                                                                                                                Length 683
                                                                                                                                DB 22;
                                                                                                                             21.4%; Score 390.5; DB 22; 30.7%; Pred. No. 1.3e-29; iive 60; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli protein sequence SEQ ID NO:330.
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Best Local Similarity 30.7%
Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-457376/49.
N-PSDB; AAH81338.
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                                                                                                     The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAM81202 to AH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in of the microorganism, inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for Xilling bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as day and approximately according to the proliferation can be used as day of the proliferation.
                                                                                                                                                                                                                                                                                                                                                                                               For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81407 encode the Escherichia coll proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491 represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 iyfvvfslvirmfnlktpgredkedeivteeansnteegltglatnyiaavggtdnlkai 409
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Novel nucleic acids encoding proteins required for Escherichia coli proliferation, useful for screening for antimicrobial agents -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 295; DB 22; 23.2%; Pred. No. 3e-20; iive 62; Mismatches 162;
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                                                                Claim 19; Page 462-463; 596pp; English
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Best Local Similarity 23.2
Matches 114; Conservative
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Antigenic protein; vaccine; Lyme disease; infection; detection
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                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 161; 275pp; English
                                                                                                                                                                                                                              Erwin AL, Hanson MS,
                                                                                                                                                                                           HUMA-) HUMAN GENOME SCI INC
                                                                                                                                           97US-0050359.
97US-0053344.
                                                                                                          98WO-US12718
                                                                                                                                97US-0057483
                                                                                                                                                                   97US-0053377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.85;
Best Local Similarity 34.88;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus bulgaricus
                                                                                                                                                                                                      (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 GPVNTYGLGEIE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 ssie-ysfgrle 127
                                  Borrelia burgdorferi.
                                                                                                                                                                                                                                                   WPI; 1999-189980/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AA;
                                                                                                                                                                                                                                                               N-PSDB; AAX61709
                                                          WO9859071-A1
                                                                                                        18-JUN-1998;
                                                                                                                                           20-JUN-1997;
                                                                                                                                03-SEP-1997;
                                                                                                                                                                   22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-2000
                                                                                  30-DEC-1998
                                                                                                                                                                                                                              Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                               sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation
                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 DAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| | | | | : :||||: | || ||: : ||:|||| | |: 58 dtvqlggegftvhverrgqvkagdplitfdadfirskdlplitpvvvsnaakfgeiegip 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 DTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYG 339
                                                                                                                                                                                                                                                                                                                                   Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                      Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to Corynebacteium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                 Phosphoenolpyruvate; sugar phosphotransferase system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 12.9%; Score 234; DB 22; Best Local Similarity 37.5%; Pred. No. 3.1e-15; Matches 51; Conservative 25; Mismatches 56;
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                      Zelder
                                                         C.glutamicum phosphoenolpyruvate protein #7.
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                                                                                                                                                                                                                                                                                                                                                                                             Claim 36; Page 142-143; 144pp; English.
                                                                                                                                                                                                                                                                                      Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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                                                                                                                                                                                                   99US-0142691.
99US-0150310.
99DE-1042095.
99DE-1042097.
                                                                                                                                                                             27-JUN-2000; 2000WO-IB00973
                                                                                                        Corynebacterium glutamicum
                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 adganssttvikvngk 133
                                                                                                                                                                                                                                                                                    Kroeger B,
                                                                                                                                                                                                                                                                                                           WPI; 2001-080989/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA;
                                                                                                                                                                                                                                                              (BADI ) BASF AG.
                                                                                                                               40200102583-A2
                                                                                                                                                                                                                23-AUG-1999;
03-SEP-1999;
                                                                                                                                                                                                                                       3-SEP-1999;
                                                                                                                                                                                                                                                                                      Pompejus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1999
                                                                                                                                                                                                     01-JUL-1999;
                                 09-APR-2001
                                                                                                                                                      11-JAN-2001
           AAB66723;
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This sequence represents a Borrella burgdorfer! (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrella genus, particularly for the use against Lyme disease in mammans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrella genus. The products can also be used for detection of members of the Borrella genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 ILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 IALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a permease encoded by the lactose operon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                          New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%; Score 233.5; DB 34.8%; Pred. No. 4.7e-15; ive 30; Mismatches 51
Lathigra R;
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AAY20013;
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                                                                                                                                                                                                          RESULT 11
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AAW28051
ID AAW2
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                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY53620-21 are encoded by the lactose operon of Lactobacillus bulgaricus, and represent a permease (AAY53620) and beta-galactosidase AAX53620). The specification describes a mutant L. bulgaricus strain lacking beta-galactosidase activity, because it has a termination (nonsense) mutation in at least one of the coding sequences of the factose operon. The resulting mutant strain unable to ferment lactose produced using it do not have to be cooled to prevent post-acidification. The mutant L. bulgaricus strain of the invention is used for producing a fermented milk product, especially yoghurt. Especially, milk is fermented with a culture of the mutant strain and optionally Streptococcus thermophilus in the presence of at least one sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mutant Lactobacillus bulgaricus strain lacking beta-galactosidase activity useful for making fermented milk products, especially yoghurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 thevksalresnekttlkgvfkvlggndgllwlafaywfyglgintlnalglyyfsyilg 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 dargysllytintfvglisasffpslakkfnrnrlfyaciavmllgigvfsvasgslals 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---L 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEV 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 221.5; DB 21; 21.8%; Pred. No. 4.4e-13; Live 66; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVCAVVTFF---IAF-----GAAIAYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 22-24; 32pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 YLVRRNGSIDPDATAAPVPA-------
                                                                                                                                                                                                                                                                                                                           Gendre F;
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                                                                                                                                                98FR-0006456.
                                                                                                                                                                                                    98FR-0006456.
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                                                                                                                                                                                                                                                                                                                        Brignon P,
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-026146/03.
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Matches 111; Conserv
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                        FR2778921-A1
                                                                                                                                             22-MAY-1998;
                                                                                                                                                                                                    22-MAY-1998;
                                                                                                                                                                                                                                                                                                                        Benbadis L,
                                                                                  26-NOV-1999
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invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can also be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GKIVVAFFSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLC 306
469 kvyapfagtvrqlaktrhsivl----enehgvlvlihlglgtvklngtgfvsyveegsqv 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a Borrelia burgdorferi (Bb) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                            Antigenic protein; vaccine; Lyme disease; infection; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 EFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIE 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 166.5; DB 2
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
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34.7%; Pred. No. 1...
'.c 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lathigra R;
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                                                                                                                                                                                                                                                                                                                                                                 burgdorferi antigenic protein, t346.aa.
                                               KAGELLCEFDIDAIKAAGYEVTTPIVVSN 328
                                                                           :||: : || ||| | : | : | |
525 eagggilefwdpaikgaklddtvivtvin 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 161; 275pp; English.
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                                                                                                                                                                                                                  AAY20013 standard; Protein; 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanson MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC.
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97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-189980/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX61710.
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22-JUL-1997;
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Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a Staphylococcus aureus protein, that, based on homology with a human or Staphylococcus aureus protein, is believed to be a nerve growth factor or ptsG protein. The DNA sequence was isolated from a library of clones of S. aureus WCHH 29 in Escherichia coli. The DNA sequence can be used in the construction of riboxymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host dagminst invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                      //octe= "residues designated X are not defined in
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S.
                                                                             Amino acid sequence of Staphylococcus aureus protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knowles DJC,
Ward JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Pages 432-433; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenberg M,
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hodgson JE,
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                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burnham MK,
Reichard RW,
                                                                                                                                                                                                                                          Misc-difference 1..126
                                                                                                                                                                                              Staphylococcus aureus.
                                                                                                                                                              coxic shock syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aureus infection
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                                             27-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pratt JM,
               AAW28051;
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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardant; thrombolytic; coagulant; vasotropic; antididabetic; hypotensive; dermatological; immunosuppressive; antididabetic; hypotensive; dermatological; antifungal; antirheumatic; antidinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 kgfkyfvngndhveagqtxlqfdqqyiqqxgynadxivvis-----nsadlgkvelt 109
                                                                                                                                                                                                                                                                                                                                                                                                                      228 LGSGVAI-VPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 THFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                 DB 18; Length 126;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                     44;
                                                                                                                                                                                                                            8.9%; Score 161.5; DB 1932.8%; Pred. No. 3.8e-08; Live 25; Mismatches 44
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Matches
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Claim 11; Page 1038; 5507pp; English.

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vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiahamatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antidianedic; gene therapy; cancer; proliferative disorder; hypotherapic, antidhyroid; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuia; burn; wound; bone damage; cartilage damage; antinflammatory disease; coaqulation;
                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                Human ORFX ORF555 polypeptide sequence SEQ ID NO:1110.
             AAB40791 standard; Protein; 108 AA.
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99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000WO-US08621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127607
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                thrombosis; contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-602362/57.
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                                                                                                                                                                                                                                                                                                                                                                       WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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05-APR-1999;
                                                                    08-FEB-2001
                                         AAB40791;
AAB40791
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                          194 PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF 253
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antlinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                                 4;
                                                                                                                                                          8.5%; Score 154; DB 21; Length 108; 32.7%; Pred. No. 1.7e-07; tive 19; Mismatches 43; Indels
to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae type 4 protein sequence #56.
                                                                                                                                                                                                                                                                                                                                                                                                                       291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY81556 standard; Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MICR-) MICROBIAL TECHNICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0016337.
99US-0125164.
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gilbert CFG, Hansbro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-195300/17.
                                                                                                                                                                                     Best Local Similarity
Matches 32; Conserv
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                                                               108 AA;
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coagulation;
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                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY81556;
                                                                                                                                                                 Query Match
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DB 21; Length 449;

8.3%; Score 150.5;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                  ----ganivfafvspialanmaenaagghfav 301
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                                                                   VGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATAS---MANIAQGAA----
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Ikeda M, Ozaki A;
         3e-06;
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                               Mismatches
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26.78; Pic
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07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
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              Local Similarity 26.7
nes 56; Conservative
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Tateishi N, Senoh A,
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                                                               Ouery Match 6.5%; Score 118.5; DB 22; Length 805; Best Local Similarity 22.8%; Pred. No. 0.0099; Matches 101; Conservative 55; Mismatches 174; Indels 113;
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Searched:

Tetraodon

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188296 MA Tetraodon tz16d08.x hb89a03.x

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BE721200 AL244017 AW173566 AI917973

SWOVAFCAP

AL071370 AI318021

AI812147

Drosophil

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14-FEB-1997
CDNA clone FB20C8, mRNA
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Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 21, 1992 this sequence version replaced gi:279156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="ATCC (inhost):86662"
/db_xref="GDB:D052785E"
/db_xref="taxon:9606"
/clone="FF20C8"
/clone="FF20C8"
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CNS025EN
AW573719
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CNS016U2
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T03017.1 GI:314258
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 March 22, 2002, 08:11:36 ; Search time 1607.29 Seconds
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7414.386 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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CNS03CVD
CNS03H6V
BE997957
CNS00L0P
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JOURNAL
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
qenome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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0
/note="Vector: Lambda ZAP II; The FB library (catalog #937201, Stratagene) was constructed by directional coloning and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 681)

1 (bases 1 to 681)

2 (bases 1 to 681)

Bouneau.L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using
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g 282 t 50 others
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                                                                                                                                            Length 473;
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/clone="262H14"
                                                                                                                                              DB 11;
                                                                                                                                            Score 45.8; DE Pred. No. 0.1; 0; Mismatches
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/organism="Tetraodon
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Tetraodon nigroviridis.
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/note="Genoscope st
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer institute in Buffalo, NY. The library is named RPCI:98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library of filters for hybridization from the BACPAC Resource Center can be filtered by the the context can be
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                214 ggccttgcaggtgcttcaggtgtctccgctgttcttggtattacggagcctgcgatcttc 273
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Location/Qualifiers
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   Length 681;
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/db_xref="taxon:7227"
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      DB 13;
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Score 41.8; DB
Pred. No. 1.3;
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/clone="BACR14B09"
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Best Local Similarity
Matches 139; Conserv
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
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University of Minnesota
Vall Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
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Fedorova.M., Plerson.B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
,C.D., Bowman.C.L., Craven,M.B., Cho,J. and Fraser,C.M.
ESTS from senescent nodules of Medicago truncatula
Unpublished (2000)
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University of Minnesota name: M271936e TIGR sequence name:
WTKAK05TKB More information is available at:
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      Length 895;
                                        Indels
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EST429681 GVSN Medicago truncatula cDNA clone
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Query Match 3.8%; Score 41.6; DB 13; Best Local Similarity 19.9%; Pred. No. 1.6; Matches 68; Conservative 115; Mismatches 159;
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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/clone_lib="GVSN"
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Fedorova,M., Plerson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng,H.L., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,J.E. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
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/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: Xhoi; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The collected from 2 month old plants at mid-pod stage. The CNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Glapapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Tel: 612 625 5715
Fax: 651-649-5058
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EST316674 GVN Medicago truncatula cDNA clone pGVN-51G2, mRNA
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Pred. No. 1.6;
); Mismatches 101;
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Department of Agronomy and Plant Genetics
University of Minnesota

    .559
        //organism="Medicago truncatula" //cultivar="genotype A17" /db_xref="taxon:880"

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TIGR sequence name:MTCAR37TK
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University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
7Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@marcon.tc.umn.edu
University of Minnesota name: M381580e TIGR sequence name:
University of Minnesota name: available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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EST482254 GVN Medicago truncatula cDNA clone pGVN-57H8 5' end, mRNA
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Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
                                                                                                                                                                          inoculation with Sinorhizobium meliloti. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
/tissue_rype="MX-fixing root nodules"
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab-host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
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Pred. No. 1.6;
0; Mismatches 101; Indels 0
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Unpublished (2001)
Contact: Carroll P. Vance
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Best Local Similarity 50.2%;
Matches 102; Conservative
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Medicago truncatula
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C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
C.D. Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M.
Contact carrol P. Vance
Contact: Carrol P. Vance
Unpublished (2000)
Contact: Carrol P. Vance
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Fax: 651-649-5058
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Xho1; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper page and propagated in XLOLR cells."

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                /tissue_type="N2-fixing root nodules" //dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti" /lab_host="E. coli strain XLOLR"
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50.2%; Pred. No. 1.7;
tive 0; Mismatches 101;
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-57H8"
/clone_lib="GVN"
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                                                                          /clone_lib="GySN"
/tissue_type="senescent root nodules"
/tissue_type="senescent root nodules from 40 day old
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
/lab_host="E. coll strain SOLR"
/note="Vector: paluescript SK +/-; Site_1: EcoRI; Site_2:
Xhoi: CDNA was prepared from polyA+ enriched RNA from the
mixture of effective nodules of 40 day old plants
harvested 36 hours post shoot removal and nodules
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cDNA was directionally ligated into the Uni-ZAP XR vector
from Stratagene and packaged using Gigapack III Gold
packaging extracts. Plasmids containing cDNA inserts were
excised from the recombinant lambda-ZAP phage using
Ex-Assist helper phage and propagated in SOLR cells."
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley brosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNSOO6UO 884 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACRI4N21 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                948 aggitatgaggiaaccacgccgaitgitgittcgaaitacaagaaaaccggaccigiaaa 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          888 cgatgaagtcaaagcaggggagctgctgtgtgaattcgatattgatgccattaaggctgc 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 TGGTTTTGTCACTGCATCTGAGTTGCATTATTACTTGACAAATCAAGGCGATTAAGGCGGAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cattggtttcgacacagtaaacctcaacggcacgcactttaacccgctgaagaagcaggg 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 CAATGAAGAAGTGAGCGACTTTGTTCGTGAGGCTGATTCTGATAGTGATGGACATCTAAG 492
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41.4; DB 11;
Pred. No. 1.7;
0; Mismatches 101;
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly), genomic survey sequence. AL065923
                                                               /clone="pGVSN-9J12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcosI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fisher, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S16 RKGKVGMVAVKTGGGGGGKRTGTKKGGKSTKGDGKKGVTGGTKKTTTKDDTTGKKTTG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggccttgcaggtgctccaggtgtctctggtattacggagcctgcgatcttc 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggcgctttgattgcactctttaatatcaaggcagttgcgttgggcgctgcaggtttcttg 393
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1 (bases 1 to 983)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 884;
                                                                                                                                                                                                                                                                                                                                                                                                                                    329 others
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                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 15.0%; Pred. No. 2.7;
Conservative 147; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 40.8; DF 15.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                 62 c
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula
Stararyota: Viridipliantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; addicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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EST429680 GVSN Medicago truncatula cDNA clone pGVSN-8B9, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 tttgattgcactctttaatatcaaggcagttgcgttgggcgctgcaggtttcttgggtgt
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                              3 (bases 1 to 970)
Genoscope
Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
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University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, 171: 612 625 5715
Fax: 651-649-5058
Email: vance004@marcon.tc.umn.edu
University of Minnesota name: M771935e TIGR sequence MTKAK05TK More information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                           l. .970
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="026011"
/clone="026011"
/clone="Genoscope sequence ID : C0BGG
/note="Genoscope sequence ID : C1BGG
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2; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40.2;
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BE997957.1 GI:10698233
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Best Local Similarity 45.9%;
Matches 130; Conservative
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Unpublished
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                           REFERENCE
AUTHORS
TITLE
JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Tetracdon nigroviridis.
Tetracdon nigroviridis.
Tetracdon nigroviridis.
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.

1 (bases 1 to 970)
1 (bases 1
                                                                                                                                       Human gene number estimate provided by genome wide analysis using
                                                         Dasilva, C., Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 970)
cost-croollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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Tetraodon nigroviridis genome survey sequence T7 end of clone
026011 of library G from Tetraodon nigroviridis, genomic survey
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                                                   Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="015D07"
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                                                                                                                                                                                         /Lissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-: Site_i: EcoRI: Site_2: Xhoi; cDNA was prepared from polyA+ enriched.RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The CDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Giapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist Helper phage and propagated in SOLR cells."
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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BACR2F02 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL067821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 CAATGAAGAAGTGAGCGACTTTGTTCGTGAGGCTGATTCTGATAGTGATGGACATCTAAG
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http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                      /organism="Medicago truncatula"
                                                                                                           /cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                      /clone-"pGVSN-8B9"
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The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Eye library. CDNA Library Preparation: M. Fatima Bonaldo. Ph.D. Clone distribution: clones will be available through Research
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please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Lisogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 9256
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 GCTGCCGTTGTTGGCGCTCCATTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTTCTGTTG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 gectgegetggeegttetteateggtateggtaeegeagetateggtggegetttgattg 346
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/db.xxef="laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR23F02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.2; DB 13;
Pred. No. 7.4;
1; Mismatches 110;
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97044477
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 104; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norway rat.
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//doc="Vector: pr73b-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: The UI-R-YO library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens) library. The driver for the subtraction consisted of a pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO, UI-R-EI, UI-R-CO) and UI-R-CI). The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-YO) was constructed as follows: PCR amplified CDNA inserts from previous library clones from which 3' ESTS had been derived were used as a driver in a hybridization with the normalized whole-eye library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-YO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW583970 714 bp mRNA EST 05-JUL-2001 ia07h02.x1 Human Pancreatic Islets Homo sapiens CDNA 3' similar to SW:RL14_HUMAN P50914 60S RIBOSOMAL PROTEIN L14 ;, mRNA sequence.
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Genetics This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1785384 The following repetitive elements were found in this cDNA sequence: 357-476, >(CAA)n#Simple_repeat 478-538, >(CAA)n#Simple_repeat Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 teggtateggtacegeagetateggtggegetttgattgeaetettaatateaaggeag 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 ttgcgttggggcgctgcaggtttcttgggtgttttttttattgatgctccagatatggtca 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 ITGTTGTTATTTCTGTTGTTGTTGTTGTTGCTGCTGTTGTTGTTATTTCTGTTGTTG 402
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Pred. No. 8.2;
0; Mismatches 87; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                /clone="UI-R-Y0-lu-g-12-0-UI"
/clone_lib="UI-R-Y0"
                                                                                                                                                                                                                                                                       /strain="Sprague-Dawley<sup>;</sup>
/db_xref="taxon:10116"
                                                                                                                                                                               Location/Qualifiers
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Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, F., Endoyrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT priming. Size-selected by column fractionation;
                                                                                                                                                                                      Endocrine Pancreas Consortium
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                          Library was constructed by Dr. Douglas Melton DNA sequencing by: washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI436816 401 bp mRNA EST 09-MAR-1999 SWOV3MCAM11A12SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM11A12 5',
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                                                                                                                   Unpublished (2000)
Other_ESTs: ia07h02.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Human Pancreatic Islets"
/tissue_type="falets of Langerhans"
/dev_stage="Adult"
/lab_host="DH108"
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47.2%; Pred. No. 8.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 304.
Location/Qualifiers
1.714
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                       dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -400P from Gibco
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AI436816
AI436816.1 GI:4284712
EST.
                                                                                                                                                                                                                                                                Tel: 617-495-1812
Fax: 617-495-8557
Email: dmeltonati
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/dev_stage="moliting L3"
//deb_host="xi1-blue MRF""
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//def="vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filatial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NTC 135 and collected after day I, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture, mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day I, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has I x 1066 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Justigman and Michalle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email:
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S Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Milliams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Milliams, S.A., Expressed in molting L3 larvae of Onchocerca volvulus Contact: Steven A. Williams

Wolbcular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
Tel: 4135833826
Fax: 413583386
Fax: 4135833786
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Fax: 10cation/Qualifiers
                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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/strain="Kumba, Cameroons"
/db_xref="taxon:6282"
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102 c 56 g
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